

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Artavanis-Tsakonas, S. et al.
- (ii) TITLE OF INVENTION: Therapeutic And Diagnostic Methods
And Compositions Based On Notch Proteins And
Nucleic Acids
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/083,590
(B) FILING DATE: 25-JUN-1993
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Misrock, S. Leslie
(B) REGISTRATION NUMBER: 18,872
(C) REFERENCE/DOCKET NUMBER: 7326-015
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212 790-9090
(B) TELEFAX: 212 8698864/9741
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2892 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 142..2640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGAG GAATTATTCA AAACATAAAC ACAATAACA ATTTGAGTAG TTGCCGCACA	60
CACACACACA CACAGCCCGT GGATTATTAC ACTAAAAGCG ACACTCAATC CAAAAAATCA	120
GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA	171

						Met 1	His	Trp	Ile	Lys 5	Cys	Leu	Leu	Thr	Ala 10	
TTC	ATT	TGC	TTC	ACA	GTC	ATC	GTG	CAG	GTT	CAC	AGT	TCC	GGC	AGC	TTT	219
Phe	Ile	Cys	Phe	Thr 15	Val	Ile	Val	Gln	Val 20	His	Ser	Ser	Gly	Ser 25	Phe	
GAG	TTG	CGC	CTG	AAG	TAC	TTC	AGC	AAC	GAT	CAC	GGG	CGG	GAC	AAC	GAG	267
Glu	Leu	Arg	Leu 30	Lys	Tyr	Phe	Ser	Asn 35	Asp	His	Gly	Arg	Asp 40	Asn	Glu	
GGT	CGC	TGC	TGC	AGC	GGG	GAG	TCG	GAC	GGA	GCG	ACG	GGC	AAG	TGC	CTG	315
Gly	Arg	Cys 45	Cys	Ser	Gly	Glu	Ser 50	Asp	Gly	Ala	Thr	Gly 55	Lys	Cys	Leu	
GGC	AGC	TGC	AAG	ACG	CGG	TTT	CGC	GTC	TGC	CTA	AAG	CAC	TAC	CAG	GCC	363
Gly	Ser 60	Cys	Lys	Thr	Arg	Phe 65	Arg	Val	Cys	Leu	Lys 70	His	Tyr	Gln	Ala	
ACC	ATC	GAC	ACC	ACC	TCC	CAG	TGC	ACC	TAC	GGG	GAC	GTG	ATC	ACG	CCC	411
Thr 75	Ile	Asp	Thr	Thr	Ser 80	Gln	Cys	Thr	Tyr	Gly 85	Asp	Val	Ile	Thr	Pro 90	
ATT	CTC	GGC	GAG	AAC	TCG	GTC	AAT	CTG	ACC	GAC	GCC	CAG	CGC	TTC	CAG	459
Ile	Leu	Gly	Glu	Asn 95	Ser	Val	Asn	Leu	Thr 100	Asp	Ala	Gln	Arg	Phe 105	Gln	
AAC	AAG	GGC	TTC	ACG	AAT	CCC	ATC	CAG	TTC	CCC	TTC	TCG	TTC	TCA	TGG	507
Asn	Lys	Gly	Phe 110	Thr	Asn	Pro	Ile	Gln 115	Phe	Pro	Phe	Ser	Phe 120	Ser	Trp	
CCG	GGT	ACC	TTC	TCG	CTG	ATC	GTC	GAG	GCC	TGG	CAT	GAT	ACG	AAC	AAT	555
Pro	Gly	Thr 125	Phe	Ser	Leu	Ile	Val 130	Glu	Ala	Trp	His	Asp 135	Thr	Asn	Asn	
AGC	GGC	AAT	GCG	CGA	ACC	AAC	AAG	CTC	CTC	ATC	CAG	CGA	CTC	TTG	GTG	603
Ser	Gly 140	Asn	Ala	Arg	Thr	Asn 145	Lys	Leu	Leu	Ile	Gln 150	Arg	Leu	Leu	Val	
CAG	CAG	GTA	CTG	GAG	GTG	TCC	TCC	GAA	TGG	AAG	ACG	AAC	AAG	TCG	GAA	651
Gln	Gln	Val	Leu	Glu	Val 160	Ser	Ser	Glu	Trp	Lys 165	Thr	Asn	Lys	Ser	Glu 170	
TCG	CAG	TAC	ACG	TCG	CTG	GAG	TAC	GAT	TTC	CGT	GTC	ACC	TGC	GAT	CTC	699
Ser	Gln	Tyr	Thr	Ser 175	Leu	Glu	Tyr	Asp	Phe 180	Arg	Val	Thr	Cys	Asp 185	Leu	
AAC	TAC	TAC	GGA	TCC	GGC	TGT	GCC	AAG	TTC	TGC	CGG	CCC	CGC	GAC	GAT	747
Asn	Tyr	Tyr	Gly 190	Ser	Gly	Cys	Ala	Lys 195	Phe	Cys	Arg	Pro	Arg 200	Asp	Asp	
TCA	TTT	GGA	CAC	TCG	ACT	TGC	TCG	GAG	ACG	GGC	GAA	ATT	ATC	TGT	TTG	795
Ser	Phe	Gly 205	His	Ser	Thr	Cys	Ser 210	Glu	Thr	Gly	Glu	Ile 215	Ile	Cys	Leu	
ACC	GGA	TGG	CAG	GGC	GAT	TAC	TGT	CAC	ATA	CCC	AAA	TGC	GCC	AAA	GGC	843
Thr	Gly 220	Trp	Gln	Gly	Asp	Tyr 225	Cys	His	Ile	Pro	Lys 230	Cys	Ala	Lys	Gly	
TGT	GAA	CAT	GGA	CAT	TGC	GAC	AAA	CCC	AAT	CAA	TGC	GTT	TGC	CAA	CTG	891
Cys	Glu	His	Gly	His	Cys 240	Asp	Lys	Pro	Asn	Gln 245	Cys	Val	Cys	Gln	Leu 250	
GGC	TGG	AAG	GGA	GCC	TTG	TGC	AAC	GAG	TGC	GTT	CTG	GAA	CCG	AAC	TGC	939
Gly	Trp	Lys	Gly	Ala 255	Leu	Cys	Asn	Glu	Cys 260	Val	Leu	Glu	Pro	Asn 265	Cys	

ATC	CAT	GGC	ACC	TGC	AAC	AAA	CCC	TGG	ACT	TGC	ATC	TGC	AAC	GAG	GGT	987
Ile	His	Gly	Thr	Cys	Asn	Lys	Pro	Trp	Thr	Cys	Ile	Cys	Asn	Glu	Gly	
			270					275						280		
TGG	GGA	GGC	TTG	TAC	TGC	AAC	CAG	GAT	CTG	AAC	TAC	TGC	ACC	AAC	CAC	1035
Trp	Gly	Gly	Leu	Tyr	Cys	Asn	Gln	Asp	Leu	Asn	Tyr	Cys	Thr	Asn	His	
		285					290					295				
AGA	CCC	TGC	AAG	AAT	GGC	GGA	ACC	TGC	TTC	AAC	ACC	GGC	GAG	GGA	TTG	1083
Arg	Pro	Cys	Lys	Asn	Gly	Gly	Thr	Cys	Phe	Asn	Thr	Gly	Glu	Gly	Leu	
	300					305					310					
TAC	ACA	TGC	AAA	TGC	GCT	CCA	GGA	TAC	AGT	GGT	GAT	GAT	TGC	GAA	AAT	1131
Tyr	Thr	Cys	Lys	Cys	Ala	Pro	Gly	Tyr	Ser	Gly	Asp	Asp	Cys	Glu	Asn	
315					320					325					330	
GAG	ATC	TAC	TCC	TGC	GAT	GCC	GAT	GTC	AAT	CCC	TGC	CAG	AAT	GGT	GGT	1179
Glu	Ile	Tyr	Ser	Cys	Asp	Ala	Asp	Val	Asn	Pro	Cys	Gln	Asn	Gly	Gly	
				335				340						345		
ACC	TGC	ATC	GAT	GAG	CCG	CAC	ACA	AAA	ACC	GGC	TAC	AAG	TGT	CAT	TGC	1227
Thr	Cys	Ile	Asp	Glu	Pro	His	Thr	Lys	Thr	Gly	Tyr	Lys	Cys	His	Cys	
			350					355					360			
GCC	AAC	GGC	TGG	AGC	GGA	AAG	ATG	TGC	GAG	GAG	AAA	GTG	CTC	ACG	TGT	1275
Ala	Asn	Gly	Trp	Ser	Gly	Lys	Met	Cys	Glu	Glu	Lys	Val	Leu	Thr	Cys	
		365					370					375				
TCG	GAC	AAA	CCC	TGT	CAT	CAG	GGA	ATC	TGC	CGC	AAC	GTT	CGT	CCT	GGC	1323
Ser	Asp	Lys	Pro	Cys	His	Gln	Gly	Ile	Cys	Arg	Asn	Val	Arg	Pro	Gly	
	380					385					390					
TTG	GGA	AGC	AAG	GGT	CAG	GGC	TAC	CAG	TGC	GAA	TGT	CCC	ATT	GGC	TAC	1371
Leu	Gly	Ser	Lys	Gly	Gln	Gly	Tyr	Gln	Cys	Glu	Cys	Pro	Ile	Gly	Tyr	
395					400					405					410	
AGC	GGA	CCC	AAC	TGC	GAT	CTC	CAG	CTG	GAC	AAC	TGC	AGT	CCG	AAT	CCA	1419
Ser	Gly	Pro	Asn	Cys	Asp	Leu	Gln	Leu	Asp	Asn	Cys	Ser	Pro	Asn	Pro	
				415				420						425		
TGC	ATA	AAC	GGT	GGA	AGC	TGT	CAG	CCG	AGC	GGA	AAG	TGT	ATT	TGC	CCA	1467
Cys	Ile	Asn	Gly	Gly	Ser	Cys	Gln	Pro	Ser	Gly	Lys	Cys	Ile	Cys	Pro	
			430					435					440			
GCG	GGA	TTT	TCG	GGA	ACG	AGA	TGC	GAG	ACC	AAC	ATT	GAC	GAT	TGT	CTT	1515
Ala	Gly	Phe	Ser	Gly	Thr	Arg	Cys	Glu	Thr	Asn	Ile	Asp	Asp	Cys	Leu	
		445					450					455				
GGC	CAC	CAG	TGC	GAG	AAC	GGA	GGC	ACC	TGC	ATA	GAT	ATG	GTC	AAC	CAA	1563
Gly	His	Gln	Cys	Glu	Asn	Gly	Gly	Thr	Cys	Ile	Asp	Met	Val	Asn	Gln	
	460					465					470					
TAT	CGC	TGC	CAA	TGC	GTT	CCC	GGT	TTC	CAT	GGC	ACC	CAC	TGT	AGT	AGC	1611
Tyr	Arg	Cys	Gln	Cys	Val	Pro	Gly	Phe	His	Gly	Thr	His	Cys	Ser	Ser	
475					480					485					490	
AAA	GTT	GAC	TTG	TGC	CTC	ATC	AGA	CCG	TGT	GCC	AAT	GGA	GGA	ACC	TGC	1659
Lys	Val	Asp	Leu	Cys	Leu	Ile	Arg	Pro	Cys	Ala	Asn	Gly	Gly	Thr	Cys	
				495				500						505		
TTG	AAT	CTC	AAC	AAC	GAT	TAC	CAG	TGC	ACC	TGT	CGT	GCG	GGA	TTT	ACT	1707
Leu	Asn	Leu	Asn	Asn	Asp	Tyr	Gln	Cys	Thr	Cys	Arg	Ala	Gly	Phe	Thr	
			510					515					520			
GGC	AAG	GAT	TGC	TCT	GTG	GAC	ATC	GAT	GAG	TGC	AGC	AGT	GGA	CCC	TGT	1755
Gly	Lys	Asp	Cys	Ser	Val	Asp	Ile	Asp	Glu	Cys	Ser	Ser	Gly	Pro	Cys	
		525					530					535				

CAT His 540	AAC Asn	GGC Gly	GGC Gly	ACT Thr	TGC Cys	ATG Met 545	AAC Asn	CGC Arg	GTC Val	AAT Asn 550	TCG Ser	TTC Phe	GAA Glu	TGC Cys	GTG Val	1803
TGT Cys 555	GCC Ala	AAT Asn	GGT Gly	TTC Phe	AGG Arg 560	GGC Gly	AAG Lys	CAG Gln	TGC Cys	GAT Asp 565	GAG Glu	GAG Glu	TCC Ser	TAC Tyr	GAT Asp 570	1851
TCG Ser	GTG Val	ACC Thr	TTC Phe	GAT Asp 575	GCC Ala	CAC His	CAA Gln	TAT Tyr	GGA Gly 580	GCG Ala	ACC Thr	ACA Thr	CAA Gln	GCG Ala 585	AGA Arg	1899
GCC Ala	GAT Asp	GGT Gly	TTG Leu 590	ACC Thr	AAT Asn	GCC Ala	CAG Gln	GTA Val 595	GTC Val	CTA Leu	ATT Ile	GCT Ala	GTT Val 600	TTC Phe	TCC Ser	1947
GTT Val	GCG Ala	ATG Met 605	CCT Pro	TTG Leu	GTG Val	GCG Ala	GTT Val 610	ATT Ile	GCG Ala	GCG Ala	TGC Cys 615	GTG Val	GTC Val	TTC Phe	TGC Cys	1995
ATG Met 620	AAG Lys	CGC Arg	AAG Lys	CGT Arg	AAG Lys	CGT Arg 625	GCT Ala	CAG Gln	GAA Glu	AAG Lys	GAC Asp 630	GAC Asp	GCG Ala	GAG Glu	GCC Ala	2043
AGG Arg 635	AAG Lys	CAG Gln	AAC Asn	GAA Glu	CAG Gln 640	AAT Asn	GCG Ala	GTG Val	GCC Ala	ACA Thr 645	ATG Met	CAT His	CAC His	AAT Asn	GGC Gly 650	2091
AGT Ser	GGG Gly	GTG Val	GGT Gly	GTA Val 655	GCT Ala	TTG Leu	GCT Ala	TCA Ser	GCC Ala 660	TCT Ser	CTG Leu	GGC Gly	GGC Gly	AAA Lys 665	ACT Thr	2139
GGC Gly	AGC Ser	AAC Asn 670	AGC Ser	GGT Gly	CTC Leu	ACC Thr	TTC Phe	GAT Asp 675	GGC Gly	GGC Gly	AAC Asn	CCG Pro	AAT Asn 680	ATC Ile	ATC Ile	2187
AAA Lys	AAC Asn 685	ACC Thr	TGG Trp	GAC Asp	AAG Lys	TCG Ser 690	GTC Val	AAC Asn	AAC Asn	ATT Ile	TGT Cys 695	GCC Ala	TCA Ser	GCA Ala	GCA Ala	2235
GCA Ala 700	GCG Ala	GCG Ala	GCG Ala	GCG Ala	GCA Ala	GCA Ala 705	GCG Ala	GCG Ala	GAC Asp	GAG Glu	TGT Cys 710	CTC Leu	ATG Met	TAC Tyr	GGC Gly	2283
GGA Gly 715	TAT Tyr	GTG Val	GCC Ala	TCG Ser 720	GTG Val	GCG Ala	GAT Asp	AAC Asn	AAC Asn	AAT Asn 725	GCC Ala	AAC Asn	TCA Ser	GAC Asp	TTT Phe 730	2331
TGT Cys	GTG Val	GCT Ala	CCG Pro	CTA Leu 735	CAA Gln	AGA Arg	GCC Ala	AAG Lys	TCG Ser 740	CAA Gln	AAG Lys	CAA Gln	CTC Leu	AAC Asn 745	ACC Thr	2379
GAT Asp	CCC Pro	ACG Thr	CTC Leu 750	ATG Met	CAC His	CGC Arg	GGT Gly	TCG Ser 755	CCG Pro	GCA Ala	GGC Gly	AGC Ser	TCA Ser 760	GCC Ala	AAG Lys	2427
GGA Gly	GCG Ala	TCT Ser 765	GGC Gly	GGA Gly	GGA Gly	CCG Pro	GGA Gly 770	GCG Ala	GCG Ala	GAG Glu	GGC Gly	AAG Lys 775	AGG Arg	ATC Ile	TCT Ser	2475
GTT Val 780	TTA Leu	GGC Gly	GAG Glu	GGT Gly	TCC Ser	TAC Tyr 785	TGT Cys	AGC Ser	CAG Gln	CGT Arg	TGG Trp 790	CCC Pro	TCG Ser	TTG Leu	GCG Ala	2523
GCG Ala 795	GCG Ala	GGA Gly	GTG Val	GCC Ala	GGA Gly 800	GCC Ala	TGT Cys	TCA Ser	TCC Ser	CAG Gln 805	CTA Leu	ATG Met	GCT Ala	GCA Ala	GCT Ala 810	2571

TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG CGA TCC GTG	2619
Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val	
815 820 825	
GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT	2670
Val Cys Gly Thr Pro His Met	
830	
AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGGTT	2730
GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTTGTTG ATTGAAGCAG TTTAGTCGTC	2790
ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG	2850
TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC	2892

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	His	Trp	Ile	Lys	Cys	Leu	Leu	Thr	Ala	Phe	Ile	Cys	Phe	Thr	Val
1				5					10					15	
Ile	Val	Gln	Val	His	Ser	Ser	Gly	Ser	Phe	Glu	Leu	Arg	Leu	Lys	Tyr
			20					25					30		
Phe	Ser	Asn	Asp	His	Gly	Arg	Asp	Asn	Glu	Gly	Arg	Cys	Cys	Ser	Gly
		35					40					45			
Glu	Ser	Asp	Gly	Ala	Thr	Gly	Lys	Cys	Leu	Gly	Ser	Cys	Lys	Thr	Arg
	50					55					60				
Phe	Arg	Val	Cys	Leu	Lys	His	Tyr	Gln	Ala	Thr	Ile	Asp	Thr	Thr	Ser
65					70				75						80
Gln	Cys	Thr	Tyr	Gly	Asp	Val	Ile	Thr	Pro	Ile	Leu	Gly	Glu	Asn	Ser
				85					90					95	
Val	Asn	Leu	Thr	Asp	Ala	Gln	Arg	Phe	Gln	Asn	Lys	Gly	Phe	Thr	Asn
			100					105					110		
Pro	Ile	Gln	Phe	Pro	Phe	Ser	Phe	Ser	Trp	Pro	Gly	Thr	Phe	Ser	Leu
		115					120					125			
Ile	Val	Glu	Ala	Trp	His	Asp	Thr	Asn	Asn	Ser	Gly	Asn	Ala	Arg	Thr
	130					135					140				
Asn	Lys	Leu	Leu	Ile	Gln	Arg	Leu	Leu	Val	Gln	Gln	Val	Leu	Glu	Val
145					150					155				160	
Ser	Ser	Glu	Trp	Lys	Thr	Asn	Lys	Ser	Glu	Ser	Gln	Tyr	Thr	Ser	Leu
				165					170					175	
Glu	Tyr	Asp	Phe	Arg	Val	Thr	Cys	Asp	Leu	Asn	Tyr	Tyr	Gly	Ser	Gly
		180						185					190		
Cys	Ala	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Ser	Phe	Gly	His	Ser	Thr
		195					200					205			

Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp
 210 215 220
 Tyr Cys His Ile Pro Lys Cys Ala Lys Gly Cys Glu His Gly His Cys
 225 230 235 240
 Asp Lys Pro Asn Gln Cys Val Cys Gln Leu Gly Trp Lys Gly Ala Leu
 245 250 255
 Cys Asn Glu Cys Val Leu Glu Pro Asn Cys Ile His Gly Thr Cys Asn
 260 265 270
 Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly Trp Gly Gly Leu Tyr Cys
 275 280 285
 Asn Gln Asp Leu Asn Tyr Cys Thr Asn His Arg Pro Cys Lys Asn Gly
 290 295 300
 Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu Tyr Thr Cys Lys Cys Ala
 305 310 315 320
 Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn Glu Ile Tyr Ser Cys Asp
 325 330 335
 Ala Asp Val Asn Pro Cys Gln Asn Gly Gly Thr Cys Ile Asp Glu Pro
 340 345 350
 His Thr Lys Thr Gly Tyr Lys Cys His Cys Ala Asn Gly Trp Ser Gly
 355 360 365
 Lys Met Cys Glu Glu Lys Val Leu Thr Cys Ser Asp Lys Pro Cys His
 370 375 380
 Gln Gly Ile Cys Arg Asn Val Arg Pro Gly Leu Gly Ser Lys Gly Gln
 385 390 395 400
 Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr Ser Gly Pro Asn Cys Asp
 405 410 415
 Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro Cys Ile Asn Gly Gly Ser
 420 425 430
 Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro Ala Gly Phe Ser Gly Thr
 435 440 445
 Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu Gly His Gln Cys Glu Asn
 450 455 460
 Gly Gly Thr Cys Ile Asp Met Val Asn Gln Tyr Arg Cys Gln Cys Val
 465 470 475 480
 Pro Gly Phe His Gly Thr His Cys Ser Ser Lys Val Asp Leu Cys Leu
 485 490 495
 Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys Leu Asn Leu Asn Asn Asp
 500 505 510
 Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr Gly Lys Asp Cys Ser Val
 515 520 525
 Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys His Asn Gly Gly Thr Cys
 530 535 540
 Met Asn Arg Val Asn Ser Phe Glu Cys Val Cys Ala Asn Gly Phe Arg
 545 550 555 560
 Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp Ser Val Thr Phe Asp Ala

565					570					575					
His	Gln	Tyr	Gly	Ala	Thr	Thr	Gln	Ala	Arg	Ala	Asp	Gly	Leu	Thr	Asn
			580					585					590		
Ala	Gln	Val	Val	Leu	Ile	Ala	Val	Phe	Ser	Val	Ala	Met	Pro	Leu	Val
		595					600					605			
Ala	Val	Ile	Ala	Ala	Cys	Val	Val	Phe	Cys	Met	Lys	Arg	Lys	Arg	Lys
	610					615					620				
Arg	Ala	Gln	Glu	Lys	Asp	Asp	Ala	Glu	Ala	Arg	Lys	Gln	Asn	Glu	Gln
625					630					635					640
Asn	Ala	Val	Ala	Thr	Met	His	His	Asn	Gly	Ser	Gly	Val	Gly	Val	Ala
				645					650					655	
Leu	Ala	Ser	Ala	Ser	Leu	Gly	Gly	Lys	Thr	Gly	Ser	Asn	Ser	Gly	Leu
			660					665					670		
Thr	Phe	Asp	Gly	Gly	Asn	Pro	Asn	Ile	Ile	Lys	Asn	Thr	Trp	Asp	Lys
		675					680					685			
Ser	Val	Asn	Asn	Ile	Cys	Ala	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala
	690					695					700				
Ala	Ala	Ala	Asp	Glu	Cys	Leu	Met	Tyr	Gly	Gly	Tyr	Val	Ala	Ser	Val
705					710					715					720
Ala	Asp	Asn	Asn	Asn	Ala	Asn	Ser	Asp	Phe	Cys	Val	Ala	Pro	Leu	Gln
			725						730					735	
Arg	Ala	Lys	Ser	Gln	Lys	Gln	Leu	Asn	Thr	Asp	Pro	Thr	Leu	Met	His
			740					745					750		
Arg	Gly	Ser	Pro	Ala	Gly	Ser	Ser	Ala	Lys	Gly	Ala	Ser	Gly	Gly	Gly
		755					760					765			
Pro	Gly	Ala	Ala	Glu	Gly	Lys	Arg	Ile	Ser	Val	Leu	Gly	Glu	Gly	Ser
	770					775					780				
Tyr	Cys	Ser	Gln	Arg	Trp	Pro	Ser	Leu	Ala	Ala	Ala	Gly	Val	Ala	Gly
785					790					795					800
Ala	Cys	Ser	Ser	Gln	Leu	Met	Ala	Ala	Ala	Ser	Ala	Ala	Gly	Ser	Gly
			805					810						815	
Ala	Gly	Thr	Ala	Gln	Gln	Gln	Arg	Ser	Val	Val	Cys	Gly	Thr	Pro	His
			820				825						830		

Met

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 442..1320

96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGTCGAG CGCCGTGCTT CGAGCGGTGA TGAGCCCCTT TTCTGTCAAC GCTAAAGATC	60
TACAAAACAT CAGCGCCTAT CAAGTGAAG TGTCAAGTGT GAACAAAACA AAAACGAGAG	120
AAGCACATAC TAAGGTCCAT ATAAATAATA AATAATAATT GTGTGTGATA ACAACATTAT	180
CCAAACAAAA CCAAACAAAA CGAAGGCAAA GTGGAGAAAA TGATACAGCA TCCAGAGTAC	240
GGCCGTTATT CAGCTATCCA GAGCAAGTGT AGTGTGGCAA AATAGAAACA AACAAAGGCA	300
CCAAAATCTG CATACTGGG CTAATTAAGG CTGCCCAGCG AATTACATT TGTGTGGTGC	360
CAATCCAGAG TGAATCCGAA ACAAACTCCA TCTAGATCGC CAACCAGCAT CACGCTCGCA	420
AACGCCCCCA GAATGTACAA A ATG TTT AGG AAA CAT TTT CGG CGA AAA CCA	471
Met Phe Arg Lys His Phe Arg Arg Lys Pro	10
1 5	
GCT ACG TCG TCG TCG TTG GAG TCA ACA ATA GAA TCA GCA GAC AGC CTG	519
Ala Thr Ser Ser Ser Leu Glu Ser Thr Ile Glu Ser Ala Asp Ser Leu	25
15 20	
GGA ATG TCC AAG AAG ACG GCG ACA AAA AGG CAG CGT CCG AGG CAT CGG	567
Gly Met Ser Lys Lys Thr Ala Thr Lys Arg Gln Arg Pro Arg His Arg	40
30 35	
GTA CCC AAA ATC GCG ACC CTG CCA TCG ACG ATC CGC GAT TGT CGA TCA	615
Val Pro Lys Ile Ala Thr Leu Pro Ser Thr Ile Arg Asp Cys Arg Ser	55
45 50	
TTA AAG TCT GCC TGC AAC TTA ATT GCT TTA ATT TTA ATA CTG TTA GTC	663
Leu Lys Ser Ala Cys Asn Leu Ile Ala Leu Ile Leu Ile Leu Leu Val	70
60 65	
CAT AAG ATA TCC GCA GCT GGT AAC TTC GAG CTG GAA ATA TTA GAA ATC	711
His Lys Ile Ser Ala Ala Gly Asn Phe Glu Leu Glu Ile Leu Glu Ile	90
75 80 85	
TCA AAT ACC AAC AGC CAT CTA CTC AAC GGC TAT TGC TGC GGC ATG CCA	759
Ser Asn Thr Asn Ser His Leu Leu Asn Gly Tyr Cys Cys Gly Met Pro	105
95 100	
GCG GAA CTT AGG GCC ACC AAG ACG ATA GGC TGC TCG CCA TGC ACG ACG	807
Ala Glu Leu Arg Ala Thr Lys Thr Ile Gly Cys Ser Pro Cys Thr Thr	120
110 115	
GCA TTC CGG CTG TGC CTG AAG GAG TAC CAG ACC ACG GAG CAG GGT GCC	855
Ala Phe Arg Leu Cys Leu Lys Glu Tyr Gln Thr Thr Glu Gln Gly Ala	135
125 130	
AGC ATA TCC ACG GGC TGT TCG TTT GGC AAC GCC ACC ACC AAG ATA CTG	903
Ser Ile Ser Thr Gly Cys Ser Phe Gly Asn Ala Thr Thr Lys Ile Leu	150
140 145	
GGT GGC TCC AGC TTT GTG CTC AGC GAT CCG GGT GTG GGA GCC ATT GTG	951
Gly Gly Ser Ser Phe Val Leu Ser Asp Pro Gly Val Gly Ala Ile Val	170
155 160 165	
CTG CCC TTT ACG TTT CGT TGG ACG AAG TCG TTT ACG CTG ATA CTG CAG	999
Leu Pro Phe Thr Phe Arg Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln	185
175 180	
GCG TTG GAT ATG TAC AAC ACA TCC TAT CCA GAT GCG GAG AGG TTA ATT	1047

Ala	Leu	Asp	Met	Tyr	Asn	Thr	Ser	Tyr	Pro	Asp	Ala	Glu	Arg	Leu	Ile		
			190					195					200				
GAG	GAA	ACA	TCA	TAC	TCG	GGC	GTG	ATA	CTG	CCG	TCG	CCG	GAG	TGG	AAG		1095
Glu	Glu	Thr	Ser	Tyr	Ser	Gly	Val	Ile	Leu	Pro	Ser	Pro	Glu	Trp	Lys		
		205					210					215					
ACG	CTG	GAC	CAC	ATC	GGG	CGG	AAC	GCG	CGG	ATC	ACC	TAC	CGT	GTC	CGG		1143
Thr	Leu	Asp	His	Ile	Gly	Arg	Asn	Ala	Arg	Ile	Thr	Tyr	Arg	Val	Arg		
	220					225					230						
GTG	CAA	TGC	GCC	GTT	ACC	TAC	TAC	AAC	ACG	ACC	TGC	ACG	ACC	TTC	TGC		1191
Val	Gln	Cys	Ala	Val	Thr	Tyr	Tyr	Asn	Thr	Thr	Cys	Thr	Thr	Phe	Cys		
235					240					245					250		
CGT	CCG	CGG	GAC	GAT	CAG	TTC	GGT	CAC	TAC	GCC	TGC	GGC	TCC	GAG	GGT		1239
Arg	Pro	Arg	Asp	Asp	Gln	Phe	Gly	His	Tyr	Ala	Cys	Gly	Ser	Glu	Gly		
				255					260					265			
CAG	AAG	CTC	TGC	CTG	AAT	GGC	TGG	CAG	GGC	GTC	AAC	TGC	GAG	GAG	GCC		1287
Gln	Lys	Leu	Cys	Leu	Asn	Gly	Trp	Gln	Gly	Val	Asn	Cys	Glu	Glu	Ala		
			270					275					280				
ATA	TGC	AAG	GCG	GGC	TGC	GAC	CCC	GTC	CAC	GGC							1320
Ile	Cys	Lys	Ala	Gly	Cys	Asp	Pro	Val	His	Gly							
		285					290										

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Arg	Lys	His	Phe	Arg	Arg	Lys	Pro	Ala	Thr	Ser	Ser	Ser	Leu		
1				5					10					15			
Glu	Ser	Thr	Ile	Glu	Ser	Ala	Asp	Ser	Leu	Gly	Met	Ser	Lys	Lys	Thr		
			20					25					30				
Ala	Thr	Lys	Arg	Gln	Arg	Pro	Arg	His	Arg	Val	Pro	Lys	Ile	Ala	Thr		
		35					40					45					
Leu	Pro	Ser	Thr	Ile	Arg	Asp	Cys	Arg	Ser	Leu	Lys	Ser	Ala	Cys	Asn		
	50					55					60						
Leu	Ile	Ala	Leu	Ile	Leu	Ile	Leu	Leu	Val	His	Lys	Ile	Ser	Ala	Ala		
65				70					75						80		
Gly	Asn	Phe	Glu	Leu	Glu	Ile	Leu	Glu	Ile	Ser	Asn	Thr	Asn	Ser	His		
			85					90					95				
Leu	Leu	Asn	Gly	Tyr	Cys	Cys	Gly	Met	Pro	Ala	Glu	Leu	Arg	Ala	Thr		
		100					105						110				
Lys	Thr	Ile	Gly	Cys	Ser	Pro	Cys	Thr	Thr	Ala	Phe	Arg	Leu	Cys	Leu		
	115						120					125					
Lys	Glu	Tyr	Gln	Thr	Thr	Glu	Gln	Gly	Ala	Ser	Ile	Ser	Thr	Gly	Cys		
	130					135					140						
Ser	Phe	Gly	Asn	Ala	Thr	Thr	Lys	Ile	Leu	Gly	Gly	Ser	Ser	Phe	Val		

145		150		155		160
Leu Ser Asp Pro Gly Val Gly Ala Ile Val Leu Pro Phe Thr Phe Arg						
		165		170		175
Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln Ala Leu Asp Met Tyr Asn						
		180		185		190
Thr Ser Tyr Pro Asp Ala Glu Arg Leu Ile Glu Glu Thr Ser Tyr Ser						
		195		200		205
Gly Val Ile Leu Pro Ser Pro Glu Trp Lys Thr Leu Asp His Ile Gly						
		210		215		220
Arg Asn Ala Arg Ile Thr Tyr Arg Val Arg Val Gln Cys Ala Val Thr						
		225		230		235
Tyr Tyr Asn Thr Thr Cys Thr Thr Phe Cys Arg Pro Arg Asp Asp Gln						
		245		250		255
Phe Gly His Tyr Ala Cys Gly Ser Glu Gly Gln Lys Leu Cys Leu Asn						
		260		265		270
Gly Trp Gln Gly Val Asn Cys Glu Glu Ala Ile Cys Lys Ala Gly Cys						
		275		280		285
Asp Pro Val His Gly						
		290				

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGTGGACTT CCTTCGTGTA TTGGTGGGAG CCCTCGGGAA CGGGGGGTAA CACTGAAAGG	60
TCGAGTACCC ATTTCCGTCA TAACGGGTTG GTCGCCCCCT AGGGGTCGGA GTCAGGTGGA	120
CGGGAGGTCG ACAACGCCCCG GGGGACGGGT GGTACATGGT GTAAGGTCTT TACCGGACCG	180
GGCAAACGGG TCACACCGAA AGGGGTGAAC GGTAAC TACG GGGTCGTCCT GCCCGTCCAT	240
CGAGTCTGGT AAGAGGGTCTG CCTTAAG	267

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCTTC CATTATACGT GACTTTTCTG AAACGTAGC CACCCTAGTG TCTCTAACTC	60
CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GTCCTTAAT	120
GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC	180
AACCCGGAAC TGAAGGCTGG CTCTCACCT CTAGGCAGAG CAGGAATTCC GAGGTGGATG	240
TGTTAGATGT GAATGTCCGT GGCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCTCC	300
GAGGAGGCAG CTCAGATTTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACA	360
TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGNC CAGACAGACC GGACTGGTGA	420
GATGGCCCTG CACCTTGCAG CCCGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA	480
TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCCGC TGTCCACTCC ATGCTGCAGT	540
GGCACGTGAT GCCAAGGTGT ATTCAGATCT GTTA	574

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCAGATTCT GATTCGCAAC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA	60
CACCCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT	120
GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTCAC TGGGCAGCTG	180
CTGTCAATAA TGTGGAGGCA ACTCTTTTGT TGTGAAAAA TGGGGCCAAC CGAGACATGC	240
AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCCG GGAGGAGCTA TAAGC	295

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCATT CAGGAGGAAA GGGTGGGGAG AGAAGCAGGC ACCCACTTTC CCGTGGCTGG	60
ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CGGAGTGCCA	120
TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA	180

100

GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG 240
CAGAGCTG 248

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACGTATCTC GAGCACAGAC AGCTGACGTA CACTTTTNNNA GTGCGAGGGA CATTCGTCCG 60
ACCAGTACGA ACATTTAGGC TCAGTACGGT AGGTCCATGG CCAAGACTAG GAGACGTAGG 120
GAGCTACAGG TCCCGCTCGC TAAACTCGGA CCACTGAAAC CTCCGGTCTGA CAGTCGGTAA 180
GCGAACAAGA GGGCCAGATC TTAGAGAAGG TGTCGCGGCG AGACTCGGGC TCGGGTCAGG 240
CGGCCTTAAG GACGTCGGGC CCNNNAGGTG ATCAAGATCT CGNCNCGGCG GCGGCCACCT 300
CGAGGNCGAA AACAAGGGAA ATC 323

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..3234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC 48
Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn
1 5 10 15
CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC 96
His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp
20 25 30
CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT 144
Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser
35 40 45
GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC 192
Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp
50 55 60
GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC 240

101

Gly 65	Phe	Asp	Cys	Gln	Arg 70	Ala	Glu	Gly	Gln	Cys 75	Asn	Pro	Leu	Tyr	Asp 80	
CAG Gln	TAC Tyr	TGC Cys	AAG Lys	GAC Asp 85	CAC His	TTC Phe	AGC Ser	GAC Asp	GGG Gly 90	CAC His	TGC Cys	GAC Asp	CAG Gln	GGC Gly 95	TGC Cys	288
AAC Asn	AGC Ser	GCG Ala	GAG Glu 100	TGC Cys	GAG Glu	TGG Trp	GAC Asp	GGG Gly 105	CTG Leu	GAC Asp	TGT Cys	GCG Ala	GAG Glu 110	CAT His	GTA Val	336
CCC Pro	GAG Glu	AGG Arg 115	CTG Leu	GCG Ala	GCC Ala	GGC Gly	ACG Thr 120	CTG Leu	GTG Val	GTG Val	GTG Val	GTG Val	CTG Leu	ATG Met	CCG Pro	384
CCG Pro	GAG Glu 130	CAG Gln	CTG Leu	CGC Arg	AAC Asn	AGC Ser 135	TCC Ser	TTC Phe	CAC His	TTC Phe	CTG Leu 140	CGG Arg	GAG Glu	CTC Leu	AGC Ser	432
CGC Arg 145	GTG Val	CTG Leu	CAC His	ACC Thr	AAC Asn 150	GTG Val	GTC Val	TTC Phe	AAG Lys	CGT Arg 155	GAC Asp	GCA Ala	CAC His	GGC Gly	CAG Gln 160	480
CAG Gln	ATG Met	ATC Ile	TTC Phe	CCC Pro 165	TAC Tyr	TAC Tyr	GGC Gly	CGC Arg	GAG Glu 170	GAG Glu	GAG Glu	CTG Leu	CGC Arg	AAG Lys 175	CAC His	528
CCC Pro	ATC Ile	AAG Lys	CGT Arg 180	GCC Ala	GCC Ala	GAG Glu	GGC Gly	TGG Trp 185	GCC Ala	GCA Ala	CCT Pro	GAC Asp	GCC Ala 190	CTG Leu	CTG Leu	576
GGC Gly	CAG Gln	GTG Val 195	AAG Lys	GCC Ala	TCG Ser	CTG Leu	CTC Leu 200	CCT Pro	GGT Gly	GGC Gly	AGC Ser	GAG Glu 205	GGT Gly	GGG Gly	CGG Arg	624
CGG Arg 210	CGG Arg	AGG Arg	GAG Glu	CTG Leu	GAC Asp	CCC Pro 215	ATG Met	GAC Asp	GTC Val	CGC Arg	GGC Gly 220	TCC Ser	ATC Ile	GTC Val	TAC Tyr	672
CTG Leu 225	GAG Glu	ATT Ile	GAC Asp	AAC Asn	CGG Arg 230	CAG Gln	TGT Cys	GTG Val	CAG Gln	GCC Ala 235	TCC Ser	TCG Ser	CAG Gln	TGC Cys	TTC Phe 240	720
CAG Gln	AGT Ser	GCC Ala	ACC Thr	GAC Asp 245	GTG Val	GCC Ala	GCA Ala	TTC Phe	CTG Leu 250	GGA Gly	GCG Ala	CTC Leu	GCC Ala	TCG Ser 255	CTG Leu	768
GGC Gly	AGC Ser	CTC Leu	AAC Asn 260	ATC Ile	CCC Pro	TAC Tyr	AAG Lys	ATC Ile 265	GAG Glu	GCC Ala	GTG Val	CAG Gln	AGT Ser 270	GAG Glu	ACC Thr	816
GTG Val	GAG Glu	CCG Pro 275	CCC Pro	CCG Pro	CCG Pro	GCG Ala	CAG Gln 280	CTG Leu	CAC His	TTC Phe	ATG Met	TAC Tyr 285	GTG Val	GCG Ala	GCG Ala	864
GCC Ala 290	GCC Ala	TTT Phe	GTG Val	CTT Leu	CTG Leu	TTC Phe 295	TTC Phe	GTG Val	GGC Gly	TGC Cys	GGG Gly 300	GTG Val	CTG Leu	CTG Leu	TCC Ser	912
CGC Arg 305	AAG Lys	CGC Arg	CGG Arg	CGG Arg	CAG Gln 310	CAT His	GGC Gly	CAG Gln	CTC Leu	TGG Trp 315	TTC Phe	CCT Pro	GAG Glu	GGC Gly	TTC Phe 320	960
AAA Lys	GTG Val	TCT Ser	GAG Glu	GCC Ala 325	AGC Ser	AAG Lys	AAG Lys	AAG Lys	CGG Arg 330	CGG Arg	GAG Glu	CCC Pro	CTC Leu	GGC Gly 335	GAG Glu	1008

GAC Asp	TCC Ser	GTG Val	GGC Gly 340	CTC Leu	AAG Lys	CCC Pro	CTG Leu	AAG Lys 345	AAC Asn	GCT Ala	TCA Ser	GAC Asp	GGT Gly 350	GCC Ala	CTC Leu	1056
ATG Met	GAC Asp	GAC Asp 355	AAC Asn	CAG Gln	AAT Asn	GAG Glu	TGG Trp 360	GGG Gly	GAC Asp	GAG Glu	GAC Asp	CTG Leu 365	GAG Glu	ACC Thr	AAG Lys	1104
AAG Lys	TTC Phe 370	CGG Arg	TTC Phe	GAG Glu	GAG Glu	CCC Pro 375	GTG Val	GTT Val	CTG Leu	CCT Pro	GAC Asp 380	CTG Leu	GAC Asp	GAC Asp	CAG Gln	1152
ACA Thr 385	GAC Asp	CAC His	CGG Arg	CAG Gln	TGG Trp 390	ACT Thr	CAG Gln	CAG Gln	CAC His	CTG Leu 395	GAT Asp	GCC Ala	GCT Ala	GAC Asp	CTG Leu 400	1200
CGC Arg	ATG Met	TCT Ser	GCC Ala	ATG Met 405	GCC Ala	CCC Pro	ACA Thr	CCG Pro 410	CCC Pro	CAG Gln	GGT Gly	GAG Glu	GTT Val	GAC Asp 415	GCC Ala	1248
GAC Asp	TGC Cys	ATG Met	GAC Asp 420	GTC Val	AAT Asn	GTC Val	CGC Arg	GGG Gly 425	CCT Pro	GAT Asp	GGC Gly	TTC Phe	ACC Thr 430	CCG Pro	CTC Leu	1296
ATG Met	ATC Ile	GCC Ala 435	TCC Ser	TGC Cys	AGC Ser	GGG Gly	GGC Gly 440	GGC Gly	CTG Leu	GAG Glu	ACG Thr	GGC Gly 445	AAC Asn	AGC Ser	GAG Glu	1344
GAA Glu 450	GAG Glu	GAG Glu	GAC Asp	GCG Ala	CCG Pro	GCC Ala 455	GTC Val	ATC Ile	TCC Ser	GAC Asp	TTC Phe 460	ATC Ile	TAC Tyr	CAG Gln	GGC Gly	1392
GCC Ala 465	AGC Ser	CTG Leu	CAC His	AAC Asn	CAG Gln 470	ACA Thr	GAC Asp	CGC Arg	ACG Thr	GGC Gly 475	GAG Glu	ACC Thr	GCC Ala	TTG Leu	CAC His 480	1440
CTG Leu	GCC Ala	GCC Ala	CGC Arg	TAC Tyr 485	TCA Ser	CGC Arg	TCT Ser	GAT Asp	GCC Ala 490	GCC Ala	AAG Lys	CGC Arg	CTG Leu 495	CTG Leu	GAG Glu	1488
GCC Ala	AGC Ser	GCA Ala	GAT Asp 500	GCC Ala	AAC Asn	ATC Ile	CAG Gln	GAC Asp 505	AAC Asn	ATG Met	GGC Gly	CGC Arg	ACC Thr 510	CCG Pro	CTG Leu	1536
CAT His	GCG Ala	GCT Ala 515	GTG Val	TCT Ser	GCC Ala	GAC Asp	GCA Ala 520	CAA Gln	GGT Gly	GTC Val	TTC Phe 525	CAG Gln	ATC Ile	CTG Leu	ATC Ile	1584
CGG Arg	AAC Asn 530	CGA Arg	GCC Ala	ACA Thr	GAC Asp	CTG Leu 535	GAT Asp	GCC Ala	CGC Arg	ATG Met	CAT His 540	GAT Asp	GGC Gly	ACG Thr	ACG Thr	1632
CCA Pro 545	CTG Leu	ATC Ile	CTG Leu	GCT Ala	GCC Ala 550	CGC Arg	CTG Leu	GCC Ala	GTG Val	GAG Glu 555	GGC Gly	ATG Met	CTG Leu	GAG Glu	GAC Asp 560	1680
CTC Leu	ATC Ile	AAC Asn	TCA Ser	CAC His 565	GCC Ala	GAC Asp	GTC Val	AAC Asn 570	GCC Ala	GTA Val	GAT Asp	GAC Asp	CTG Leu 575	GGC Gly	AAG Lys	1728
TCC Ser	GCC Ala	CTG Leu	CAC His 580	TGG Trp	GCC Ala	GCC Ala	GCC Ala	GTG Val 585	AAC Asn	AAT Asn	GTG Val	GAT Asp	GCC Ala 590	GCA Ala	GTT Val	1776
GTG Val	CTC Leu	CTG Leu 595	AAG Lys	AAC Asn	GGG Gly	GCT Ala	AAC Asn 600	AAA Lys	GAT Asp	ATG Met	CAG Gln	AAC Asn 605	AAC Asn	AGG Arg	GAG Glu	1824

GAG Glu 610	ACA Thr 610	CCC Pro 610	CTG Leu 610	TTT Phe 610	CTG Leu 615	GCC Ala 615	GCC Ala 615	CGG Arg 615	GAG Glu 620	GGC Gly 620	AGC Ser 620	TAC Tyr 620	GAG Glu 620	ACC Thr 620	GCC Ala 620	1872
AAG Lys 625	GTG Val 625	CTG Leu 625	CTG Leu 625	GAC Asp 630	CAC His 630	TTT Phe 630	GCC Ala 630	AAC Asn 630	CGG Arg 635	GAC Asp 635	ATC Ile 635	ACG Thr 635	GAT Asp 635	CAT His 640	ATG Met 640	1920
GAC Asp 645	CGC Arg 645	CTG Leu 645	CCG Pro 645	CGC Arg 645	GAC Asp 645	ATC Ile 645	GCA Ala 645	CAG Gln 645	GAG Glu 650	CGC Arg 650	ATG Met 650	CAT His 655	CAC His 655	GAC Asp 655	ATC Ile 655	1968
GTG Val 660	AGG Arg 660	CTG Leu 660	CTG Leu 660	GAC Asp 660	GAG Glu 660	TAC Tyr 660	AAC Asn 665	CTG Leu 665	GTG Val 665	CGC Arg 665	AGC Ser 665	CCG Pro 670	CAG Gln 670	CTG Leu 670	CAC His 670	2016
GGA Gly 675	GCC Ala 675	CCG Pro 675	CTG Leu 675	GGG Gly 675	GGC Gly 675	ACG Thr 680	CCC Pro 680	ACC Thr 680	CTG Leu 680	TCG Ser 680	CCC Pro 685	CCG Pro 685	CTC Leu 685	TGC Cys 685	TCG Ser 685	2064
CCC Pro 690	AAC Asn 690	GGC Gly 690	TAC Tyr 690	CTG Leu 690	GGC Gly 695	AGC Ser 695	CTC Leu 695	AAG Lys 695	CCC Pro 695	GGC Gly 700	GTG Val 700	CAG Gln 700	GGC Gly 700	AAG Lys 700	AAG Lys 700	2112
GTC Val 705	CGC Arg 705	AAG Lys 705	CCC Pro 705	AGC Ser 710	AGC Ser 710	AAA Lys 710	GGC Gly 710	CTG Leu 710	GCC Ala 715	TGT Cys 715	GGA Gly 715	AGC Ser 715	AAG Lys 715	GAG Glu 720	GCC Ala 720	2160
AAG Lys 725	GAC Asp 725	CTC Leu 725	AAG Lys 725	GCA Ala 725	CGG Arg 725	AGG Arg 725	AAG Lys 730	AAG Lys 730	TCC Ser 730	CAG Gln 730	GAT Asp 730	GGC Gly 735	AAG Lys 735	GGC Gly 735	TGC Cys 735	2208
CTG Leu 740	CTG Leu 740	GAC Asp 740	AGC Ser 740	TCC Ser 740	GGC Gly 740	ATG Met 745	CTC Leu 745	TCG Ser 745	CCC Pro 745	GTG Val 745	GAC Asp 745	TCC Ser 750	CTG Leu 750	GAG Glu 750	TCA Ser 750	2256
CCC Pro 755	CAT His 755	GGC Gly 755	TAC Tyr 755	CTG Leu 755	TCA Ser 760	GAC Asp 760	GTG Val 760	GCC Ala 760	TCG Ser 760	CCG Pro 760	CCA Pro 765	CTG Leu 765	CTG Leu 765	CCC Pro 765	TCC Ser 765	2304
CCG Pro 770	TTC Phe 770	CAG Gln 770	CAG Gln 770	TCT Ser 775	CCG Pro 775	TCC Ser 775	GTG Val 775	CCC Pro 775	CTC Leu 780	AAC Asn 780	CAC His 780	CTG Leu 780	CCT Pro 780	GGG Gly 780	ATG Met 780	2352
CCC Pro 785	GAC Asp 785	ACC Thr 785	CAC His 785	CTG Leu 790	GGC Gly 790	ATC Ile 790	GGG Gly 790	CAC His 795	CTG Leu 795	AAC Asn 795	GTG Val 795	GCG Ala 795	GCC Ala 795	AAG Lys 800	CCC Pro 800	2400
GAG Glu 805	ATG Met 805	GCG Ala 805	GCG Ala 805	CTG Leu 805	GGT Gly 805	GGG Gly 805	GGC Gly 810	GGC Gly 810	CGG Arg 810	CTG Leu 810	GCC Ala 810	TTT Phe 815	GAG Glu 815	ACT Thr 815	GGC Gly 815	2448
CCA Pro 820	CCT Pro 820	CGT Arg 820	CTC Leu 820	TCC Ser 820	CAC His 825	CTG Leu 825	CCT Pro 825	GTG Val 825	GCC Ala 825	TCT Ser 825	GGC Gly 830	ACC Thr 830	AGC Ser 830	ACC Thr 830	GTC Val 830	2496
CTG Leu 835	GGC Gly 835	TCC Ser 835	AGC Ser 835	AGC Ser 835	GGA Gly 840	GGG Gly 840	GCC Ala 840	CTG Leu 840	AAT Asn 840	TTC Phe 845	ACT Thr 845	GTG Val 845	GGC Gly 845	GGG Gly 845	TCC Ser 845	2544
ACC Thr 850	AGT Ser 850	TTG Leu 850	AAT Asn 850	GGT Gly 855	CAA Gln 855	TGC Cys 855	GAG Glu 855	TGG Trp 855	CTG Leu 860	TCC Ser 860	CGG Arg 860	CTG Leu 860	CAG Gln 860	AGC Ser 860	GGC Gly 860	2592
ATG Met 865	GTG Val 865	CCG Pro 865	AAC Asn 865	CAA Gln 870	TAC Tyr 870	AAC Asn 870	CCT Pro 870	CTG Leu 870	CGG Arg 875	GGG Gly 875	AGT Ser 875	GTG Val 875	GCA Ala 875	CCA Pro 880	GGC Gly 880	2640

CCC	CTG	AGC	ACA	CAG	GCC	CCC	TCC	CTG	CAG	CAT	GGC	ATG	GTA	GGC	CCG	2688
Pro	Leu	Ser	Thr	Gln	Ala	Pro	Ser	Leu	Gln	His	Gly	Met	Val	Gly	Pro	
				885					890					895		
CTG	CAC	AGT	AGC	CTT	GCT	GCC	AGC	GCC	CTG	TCC	CAG	ATG	ATG	AGC	TAC	2736
Leu	His	Ser	Ser	Leu	Ala	Ala	Ser	Ala	Leu	Ser	Gln	Met	Met	Ser	Tyr	
			900					905					910			
CAG	GGC	CTG	CCC	AGC	ACC	CGG	CTG	GCC	ACC	CAG	CCT	CAC	CTG	GTG	CAG	2784
Gln	Gly	Leu	Pro	Ser	Thr	Arg	Leu	Ala	Thr	Gln	Pro	His	Leu	Val	Gln	
		915					920					925				
ACC	CAG	CAG	GTG	CAG	CCA	CAA	AAC	TTA	CAG	ATG	CAG	CAG	CAG	AAC	CTG	2832
Thr	Gln	Gln	Val	Gln	Pro	Gln	Asn	Leu	Gln	Met	Gln	Gln	Gln	Asn	Leu	
	930					935					940					
CAG	CCA	GCA	AAC	ATC	CAG	CAG	CAG	CAA	AGC	CTG	CAG	CCG	CCA	CCA	CCA	2880
Gln	Pro	Ala	Asn	Ile	Gln	Gln	Gln	Gln	Ser	Leu	Gln	Pro	Pro	Pro	Pro	
945					950					955					960	
CCA	CCA	CAG	CCG	CAC	CTT	GGC	GTG	AGC	TCA	GCA	GCC	AGC	GGC	CAC	CTG	2928
Pro	Pro	Gln	Pro	His	Leu	Gly	Val	Ser	Ser	Ala	Ala	Ser	Gly	His	Leu	
				965					970					975		
GGC	CGG	AGC	TTC	CTG	AGT	GGA	GAG	CCG	AGC	CAG	GCA	GAC	GTG	CAG	CCA	2976
Gly	Arg	Ser	Phe	Leu	Ser	Gly	Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro	
			980					985					990			
CTG	GGC	CCC	AGC	AGC	CTG	GCG	GTG	CAC	ACT	ATT	CTG	CCC	CAG	GAG	AGC	3024
Leu	Gly	Pro	Ser	Ser	Leu	Ala	Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser	
		995					1000					1005				
CCC	GCC	CTG	CCC	ACG	TCG	CTG	CCA	TCC	TCG	CTG	GTC	CCA	CCC	GTG	ACC	3072
Pro	Ala	Leu	Pro	Thr	Ser	Leu	Pro	Ser	Ser	Leu	Val	Pro	Pro	Val	Thr	
	1010					1015					1020					
GCA	GCC	CAG	TTC	CTG	ACG	CCC	CCC	TCG	CAG	CAC	AGC	TAC	TCC	TCG	CCT	3120
Ala	Ala	Gln	Phe	Leu	Thr	Pro	Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro	
1025					1030					1035					1040	
GTG	GAC	AAC	ACC	CCC	AGC	CAC	CAG	CTA	CAG	GTG	CCT	GTT	CCT	GTA	ATG	3168
Val	Asp	Asn	Thr	Pro	Ser	His	Gln	Leu	Gln	Val	Pro	Val	Pro	Val	Met	
				1045				1050						1055		
GTA	ATG	ATC	CGA	TCT	TCG	GAT	CCT	TCT	AAA	GGC	TCA	TCA	ATT	TTG	ATC	3216
Val	Met	Ile	Arg	Ser	Ser	Asp	Pro	Ser	Lys	Gly	Ser	Ser	Ile	Leu	Ile	
			1060					1065					1070			
GAA	GCT	CCC	GAC	TCA	TGG											3234
Glu	Ala	Pro	Asp	Ser	Trp											
		1075														

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn
 1 5 10 15

105

His	Ala	Cys	Gly	Trp	Asp	Gly	Gly	Asp	Cys	Ser	Leu	Asn	Phe	Asn	Asp
			20					25					30		
Pro	Trp	Lys	Asn	Cys	Thr	Gln	Ser	Leu	Gln	Cys	Trp	Lys	Tyr	Phe	Ser
		35					40					45			
Asp	Gly	His	Cys	Asp	Ser	Gln	Cys	Asn	Ser	Ala	Gly	Cys	Leu	Phe	Asp
	50					55					60				
Gly	Phe	Asp	Cys	Gln	Arg	Ala	Glu	Gly	Gln	Cys	Asn	Pro	Leu	Tyr	Asp
65					70					75					80
Gln	Tyr	Cys	Lys	Asp	His	Phe	Ser	Asp	Gly	His	Cys	Asp	Gln	Gly	Cys
				85					90					95	
Asn	Ser	Ala	Glu	Cys	Glu	Trp	Asp	Gly	Leu	Asp	Cys	Ala	Glu	His	Val
			100					105					110		
Pro	Glu	Arg	Leu	Ala	Ala	Gly	Thr	Leu	Val	Val	Val	Val	Leu	Met	Pro
		115					120					125			
Pro	Glu	Gln	Leu	Arg	Asn	Ser	Ser	Phe	His	Phe	Leu	Arg	Glu	Leu	Ser
		130				135					140				
Arg	Val	Leu	His	Thr	Asn	Val	Val	Phe	Lys	Arg	Asp	Ala	His	Gly	Gln
145					150					155					160
Gln	Met	Ile	Phe	Pro	Tyr	Tyr	Gly	Arg	Glu	Glu	Glu	Leu	Arg	Lys	His
				165					170					175	
Pro	Ile	Lys	Arg	Ala	Ala	Glu	Gly	Trp	Ala	Ala	Pro	Asp	Ala	Leu	Leu
			180					185					190		
Gly	Gln	Val	Lys	Ala	Ser	Leu	Leu	Pro	Gly	Gly	Ser	Glu	Gly	Gly	Arg
		195					200					205			
Arg	Arg	Arg	Glu	Leu	Asp	Pro	Met	Asp	Val	Arg	Gly	Ser	Ile	Val	Tyr
	210					215					220				
Leu	Glu	Ile	Asp	Asn	Arg	Gln	Cys	Val	Gln	Ala	Ser	Ser	Gln	Cys	Phe
225					230					235					240
Gln	Ser	Ala	Thr	Asp	Val	Ala	Ala	Phe	Leu	Gly	Ala	Leu	Ala	Ser	Leu
				245					250					255	
Gly	Ser	Leu	Asn	Ile	Pro	Tyr	Lys	Ile	Glu	Ala	Val	Gln	Ser	Glu	Thr
			260					265					270		
Val	Glu	Pro	Pro	Pro	Pro	Ala	Gln	Leu	His	Phe	Met	Tyr	Val	Ala	Ala
		275					280					285			
Ala	Ala	Phe	Val	Leu	Leu	Phe	Phe	Val	Gly	Cys	Gly	Val	Leu	Leu	Ser
	290					295					300				
Arg	Lys	Arg	Arg	Arg	Gln	His	Gly	Gln	Leu	Trp	Phe	Pro	Glu	Gly	Phe
305					310					315					320
Lys	Val	Ser	Glu	Ala	Ser	Lys	Lys	Lys	Arg	Arg	Glu	Pro	Leu	Gly	Glu
				325					330					335	
Asp	Ser	Val	Gly	Leu	Lys	Pro	Leu	Lys	Asn	Ala	Ser	Asp	Gly	Ala	Leu
			340					345					350		
Met	Asp	Asp	Asn	Gln	Asn	Glu	Trp	Gly	Asp	Glu	Asp	Leu	Glu	Thr	Lys
	355						360					365			
Lys	Phe	Arg	Phe	Glu	Glu	Pro	Val	Val	Leu	Pro	Asp	Leu	Asp	Asp	Gln

106

370					375					380					
Thr	Asp	His	Arg	Gln	Trp	Thr	Gln	Gln	His	Leu	Asp	Ala	Ala	Asp	Leu
385					390					395					400
Arg	Met	Ser	Ala	Met	Ala	Pro	Thr	Pro	Pro	Gln	Gly	Glu	Val	Asp	Ala
				405					410					415	
Asp	Cys	Met	Asp	Val	Asn	Val	Arg	Gly	Pro	Asp	Gly	Phe	Thr	Pro	Leu
			420					425					430		
Met	Ile	Ala	Ser	Cys	Ser	Gly	Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu
		435					440					445			
Glu	Glu	Glu	Asp	Ala	Pro	Ala	Val	Ile	Ser	Asp	Phe	Ile	Tyr	Gln	Gly
	450					455					460				
Ala	Ser	Leu	His	Asn	Gln	Thr	Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His
465					470					475					480
Leu	Ala	Ala	Arg	Tyr	Ser	Arg	Ser	Asp	Ala	Ala	Lys	Arg	Leu	Leu	Glu
				485					490					495	
Ala	Ser	Ala	Asp	Ala	Asn	Ile	Gln	Asp	Asn	Met	Gly	Arg	Thr	Pro	Leu
			500					505					510		
His	Ala	Ala	Val	Ser	Ala	Asp	Ala	Gln	Gly	Val	Phe	Gln	Ile	Leu	Ile
		515					520					525			
Arg	Asn	Arg	Ala	Thr	Asp	Leu	Asp	Ala	Arg	Met	His	Asp	Gly	Thr	Thr
	530					535					540				
Pro	Leu	Ile	Leu	Ala	Ala	Arg	Leu	Ala	Val	Glu	Gly	Met	Leu	Glu	Asp
545					550					555					560
Leu	Ile	Asn	Ser	His	Ala	Asp	Val	Asn	Ala	Val	Asp	Asp	Leu	Gly	Lys
				565					570					575	
Ser	Ala	Leu	His	Trp	Ala	Ala	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Val
			580					585					590		
Val	Leu	Leu	Lys	Asn	Gly	Ala	Asn	Lys	Asp	Met	Gln	Asn	Asn	Arg	Glu
		595					600					605			
Glu	Thr	Pro	Leu	Phe	Leu	Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Thr	Ala
	610					615					620				
Lys	Val	Leu	Leu	Asp	His	Phe	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met
625					630					635					640
Asp	Arg	Leu	Pro	Arg	Asp	Ile	Ala	Gln	Glu	Arg	Met	His	His	Asp	Ile
				645					650					655	
Val	Arg	Leu	Leu	Asp	Glu	Tyr	Asn	Leu	Val	Arg	Ser	Pro	Gln	Leu	His
			660					665					670		
Gly	Ala	Pro	Leu	Gly	Gly	Thr	Pro	Thr	Leu	Ser	Pro	Pro	Leu	Cys	Ser
		675					680					685			
Pro	Asn	Gly	Tyr	Leu	Gly	Ser	Leu	Lys	Pro	Gly	Val	Gln	Gly	Lys	Lys
	690					695					700				
Val	Arg	Lys	Pro	Ser	Ser	Lys	Gly	Leu	Ala	Cys	Gly	Ser	Lys	Glu	Ala
705					710					715					720
Lys	Asp	Leu	Lys	Ala	Arg	Arg	Lys	Lys	Ser	Gln	Asp	Gly	Lys	Gly	Cys
				725					730					735	

(07)

Leu	Leu	Asp	Ser	Ser	Gly	Met	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser
			740					745					750		
Pro	His	Gly	Tyr	Leu	Ser	Asp	Val	Ala	Ser	Pro	Pro	Leu	Leu	Pro	Ser
		755					760					765			
Pro	Phe	Gln	Gln	Ser	Pro	Ser	Val	Pro	Leu	Asn	His	Leu	Pro	Gly	Met
	770					775					780				
Pro	Asp	Thr	His	Leu	Gly	Ile	Gly	His	Leu	Asn	Val	Ala	Ala	Lys	Pro
785					790					795					800
Glu	Met	Ala	Ala	Leu	Gly	Gly	Gly	Gly	Arg	Leu	Ala	Phe	Glu	Thr	Gly
				805					810					815	
Pro	Pro	Arg	Leu	Ser	His	Leu	Pro	Val	Ala	Ser	Gly	Thr	Ser	Thr	Val
			820					825					830		
Leu	Gly	Ser	Ser	Ser	Gly	Gly	Ala	Leu	Asn	Phe	Thr	Val	Gly	Gly	Ser
		835					840					845			
Thr	Ser	Leu	Asn	Gly	Gln	Cys	Glu	Trp	Leu	Ser	Arg	Leu	Gln	Ser	Gly
	850					855					860				
Met	Val	Pro	Asn	Gln	Tyr	Asn	Pro	Leu	Arg	Gly	Ser	Val	Ala	Pro	Gly
865					870					875					880
Pro	Leu	Ser	Thr	Gln	Ala	Pro	Ser	Leu	Gln	His	Gly	Met	Val	Gly	Pro
				885					890					895	
Leu	His	Ser	Ser	Leu	Ala	Ala	Ser	Ala	Leu	Ser	Gln	Met	Met	Ser	Tyr
			900					905					910		
Gln	Gly	Leu	Pro	Ser	Thr	Arg	Leu	Ala	Thr	Gln	Pro	His	Leu	Val	Gln
		915					920					925			
Thr	Gln	Gln	Val	Gln	Pro	Gln	Asn	Leu	Gln	Met	Gln	Gln	Gln	Asn	Leu
	930					935					940				
Gln	Pro	Ala	Asn	Ile	Gln	Gln	Gln	Gln	Ser	Leu	Gln	Pro	Pro	Pro	Pro
945					950					955					960
Pro	Pro	Gln	Pro	His	Leu	Gly	Val	Ser	Ser	Ala	Ala	Ser	Gly	His	Leu
				965					970					975	
Gly	Arg	Ser	Phe	Leu	Ser	Gly	Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro
			980					985					990		
Leu	Gly	Pro	Ser	Ser	Leu	Ala	Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser
		995					1000					1005			
Pro	Ala	Leu	Pro	Thr	Ser	Leu	Pro	Ser	Ser	Leu	Val	Pro	Pro	Val	Thr
	1010					1015					1020				
Ala	Ala	Gln	Phe	Leu	Thr	Pro	Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro
1025					1030					1035					1040
Val	Asp	Asn	Thr	Pro	Ser	His	Gln	Leu	Gln	Val	Pro	Val	Pro	Val	Met
				1045					1050					1055	
Val	Met	Ile	Arg	Ser	Ser	Asp	Pro	Ser	Lys	Gly	Ser	Ser	Ile	Leu	Ile
			1060					1065					1070		
Glu	Ala	Pro	Asp	Ser	Trp										
			1075												

(2) INFORMATION FOR SEQ ID NO:12:

108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

G GAG GTG GAT GTG TTA GAT GTG AAT GTC CGT GGC CCA GAT GGC TGC	46
Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys	
1 5 10 15	
ACC CCA TTG ATG TTG GCT TCT CTC CGA GGA GGC AGC TCA GAT TTG AGT	94
Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser	
20 25 30	
GAT GAA GAT GAA GAT GCA GAG GAC TCT TCT GCT AAC ATC ATC ACA GAC	142
Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp	
35 40 45	
TTG GTC TAC CAG GGT GCC AGC CTC CAG GCC CAG ACA GAC CGG ACT GGT	190
Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly	
50 55 60	
GAG ATG GCC CTG CAC CTT GCA GCC CGC TAC TCA CGG GCT GAT GCT GCC	238
Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala	
65 70 75	
AAG CGT CTC CTG GAT GCA GGT GCA GAT GCC AAT GCC CAG GAC AAC ATG	286
Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met	
80 85 90 95	
GGC CGC TGT CCA CTC CAT GCT GCA GTG GCA GCT GAT GCC CAA GGT GTC	334
Gly Arg Cys Pro Leu His Ala Ala Val Ala Asp Ala Gln Gly Val	
100 105 110	
TTC CAG ATT CTG ATT CGC AAC CGA GTA ACT GAT CTA GAT GCC AGG ATG	382
Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met	
115 120 125	
AAT GAT GGT ACT ACA CCC CTG ATC CTG GCT GCC CGC CTG GCT GTG GAG	430
Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu	
130 135 140	
GGA ATG GTG GCA GAA CTG ATC AAC TGC CAA GCG GAT GTG AAT GCA GTG	478
Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val	
145 150 155	
GAT GAC CAT GGA AAA TCT GCT CTT CAC TGG GCA GCT GCT GTC AAT AAT	526
Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn	
160 165 170 175	
GTG GAG GCA ACT CTT TTG TTG TTG AAA AAT GGG GCC AAC CGA GAC ATG	574
Val Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met	
180 185 190	
CAG GAC AAC AAG GAA GAG ACA CCT CTG TTT CTT GCT GCC CGG GAG GGG	622
Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly	
195 200 205	

AGC Ser	TAT Tyr	GAA Glu 210	GCA Ala	GCC Ala	AAG Lys	ATC Ile	CTG Leu 215	TTA Leu	GAC Asp	CAT His	TTT Phe	GCC Ala 220	AAT Asn	CGA Arg	GAC Asp	670
ATC Ile	ACA Thr 225	GAC Asp	CAT His	ATG Met	GAT Asp	CGT Arg 230	CTT Leu	CCC Pro	CGG Arg	GAT Asp	GTG Val 235	GCT Ala	CGG Arg	GAT Asp	CGC Arg	718
ATG Met 240	CAC His	CAT His	GAC Asp	ATT Ile	GTG Val 245	CGC Arg	CTT Leu	CTG Leu	GAT Asp	GAA Glu 250	TAC Tyr	AAT Asn	GTG Val	ACC Thr	CCA Pro 255	766
AGC Ser	CCT Pro	CCA Pro	GGC Gly	ACC Thr 260	GTG Val	TTG Leu	ACT Thr	TCT Ser	GCT Ala 265	CTC Leu	TCA Ser	CCT Pro	GTC Val	ATC Ile 270	TGT Cys	814
GGG Gly	CCC Pro	AAC Asn 275	AGA Arg	TCT Ser	TTC Phe	CTC Leu	AGC Ser 280	CTG Leu	AAG Lys	CAC His	ACC Thr	CCA Pro	ATG Met 285	GGC Gly	AAG Lys	862
AAG Lys	TCT Ser 290	AGA Arg	CGG Arg	CCC Pro	AGT Ser	GCC Ala	AAG Lys 295	AGT Ser	ACC Thr	ATG Met	CCT Pro 300	ACT Thr	AGC Ser	CTC Leu	CCT Pro	910
AAC Asn 305	CTT Leu	GCC Ala	AAG Lys	GAG Glu	GCA Ala	AAG Lys 310	GAT Asp	GCC Ala	AAG Lys	GGT Gly	AGT Ser 315	AGG Arg	AGG Arg	AAG Lys	AAG Lys	958
TCT Ser 320	CTG Leu	AGT Ser	GAG Glu	AAG Lys	GTC Val 325	CAA Gln	CTG Leu	TCT Ser	GAG Glu	AGT Ser 330	TCA Ser	GTA Val	ACT Thr	TTA Leu	TCC Ser 335	1006
CCT Pro	GTT Val	GAT Asp	TCC Ser	CTA Leu 340	GAA Glu	TCT Ser	CCT Pro	CAC His	ACG Thr 345	TAT Tyr	GTT Val	TCC Ser	GAC Asp	ACC Thr 350	ACA Thr	1054
TCC Ser	TCT Ser	CCA Pro	ATG Met 355	ATT Ile	ACA Thr	TCC Ser	CCT Pro	GGG Gly 360	ATC Ile	TTA Leu	CAG Gln	GCC Ala	TCA Ser 365	CCC Pro	AAC Asn	1102
CCT Pro	ATG Met 370	TTG Leu	GCC Ala	ACT Thr	GCC Ala	GCC Ala	CCT Pro 375	CCT Pro	GCC Ala	CCA Pro	GTC Val	CAT His 380	GCC Ala	CAG Gln	CAT His	1150
GCA Ala 385	CTA Leu	TCT Ser	TTT Phe	TCT Ser	AAC Asn	CTT Leu 390	CAT His	GAA Glu	ATG Met	CAG Gln	CCT Pro 395	TTG Leu	GCA Ala	CAT His	GGG Gly	1198
GCC Ala 400	AGC Ser	ACT Thr	GTG Val	CTT Leu	CCC Pro 405	TCA Ser	GTG Val	AGC Ser	CAG Gln	TTG Leu 410	CTA Leu	TCC Ser	CAC His	CAC His	CAC His 415	1246
ATT Ile	GTG Val	TCT Ser	CCA Pro	GGC Gly 420	AGT Ser	GGC Gly	AGT Ser	GCT Ala	GGA Gly 425	AGC Ser	TTG Leu	AGT Ser	AGG Arg	CTC Leu 430	CAT His	1294
CCA Pro	GTC Val	CCA Pro	GTC Val 435	CCA Pro	GCA Ala	GAT Asp	TGG Trp 440	ATG Met	AAC Asn	CGC Arg	ATG Met	GAG Glu	GTG Val 445	AAT Asn	GAG Glu	1342
ACC Thr	CAG Gln 450	TAC Tyr	AAT Asn	GAG Glu	ATG Met	TTT Phe	GGT Gly 455	ATG Met	GTC Val	CTG Leu	GCT Ala	CCA Pro 460	GCT Ala	GAG Glu	GGC Gly	1390
ACC Thr 465	CAT His	CCT Pro	GGC Gly	ATA Ile	GCT Ala	CCC Pro 470	CAG Gln	AGC Ser	AGG Arg	CCA Pro	CCT Pro 475	GAA Glu	GGG Gly	AAG Lys	CAC His	1438

(10)

ATA Ile 480	ACC Thr	ACC Thr	CCT Pro	CGG Arg	GAG Glu 485	CCC Pro	TTG Leu	CCC Pro	CCC Pro	ATT Ile 490	GTG Val	ACT Thr	TTC Phe	CAG Gln	CTC Leu 495	1486
ATC Ile	CCT Pro	AAA Lys	GGC Gly	AGT Ser 500	ATT Ile	GCC Ala	CAA Gln	CCA Pro	GCG Ala 505	GGG Gly	GCT Ala	CCC Pro	CAG Gln	CCT Pro 510	CAG Gln	1534
TCC Ser	ACC Thr	TGC Cys	CCT Pro 515	CCA Pro	GCT Ala	GTT Val	GCG Ala	GGC Gly 520	CCC Pro	CTG Leu	CCC Pro	ACC Thr	ATG Met 525	TAC Tyr	CAG Gln	1582
ATT Ile	CCA Pro	GAA Glu 530	ATG Met	GCC Ala	CGT Arg	TTG Leu	CCC Pro 535	AGT Ser	GTG Val	GCT Ala	TTC Phe	CCC Pro	ACT Thr 540	GCC Ala	ATG Met	1630
ATG Met 545	CCC Pro	CAG Gln	CAG Gln	GAC Asp	GGG Gly 550	CAG Gln	GTA Val	GCT Ala	CAG Gln	ACC Thr	ATT Ile 555	CCC Leu	CCA Pro	GCC Ala	TAT Tyr	1678
CAT His 560	CCT Pro	TTC Phe	CCA Pro	GCC Ala	TCT Ser 565	GTG Val	GGC Gly	AAG Lys	TAC Tyr	CCC Pro 570	ACA Thr	CCC Pro	CCT Pro	TCA Ser	CAG Gln 575	1726
CAC His	AGT Ser	TAT Tyr	GCT Ala	TCC Ser 580	TCA Ser	AAT Asn	GCT Ala	GCT Ala	GAG Glu 585	CGA Arg	ACA Thr	CCC Pro	AGT Ser	CAC His 590	AGT Ser	1774
GGT Gly	CAC His	CTC Leu	CAG Gln 595	GGT Gly	GAG Glu	CAT His	CCC Pro	TAC Tyr 600	CTG Leu	ACA Thr	CCA Pro	TCC Ser	CCA Pro 605	GAG Glu	TCT Ser	1822
CCT Pro	GAC Asp	CAG Gln 610	TGG Trp	TCA Ser	AGT Ser	TCA Ser	TCA Ser 615	CCC Pro	CAC His	TCT Ser	GCT Ala	TCT Ser	GAC Asp 620	TGG Trp	TCA Ser	1870
GAT Asp 625	GTG Val	ACC Thr	ACC Thr	AGC Ser	CCT Pro	ACC Thr 630	CCT Pro	GGG Gly	GGT Gly	GCT Ala	GGA Gly 635	GGA Gly	GGT Gly	CAG Gln	CGG Arg	1918
GGA Gly 640	CCT Pro	GGG Gly	ACA Thr	CAC His	ATG Met 645	TCT Ser	GAG Glu	CCA Pro	CCA Pro	CAC His 650	AAC Asn	AAC Asn	ATG Met	CAG Gln 655	GTT Val	1966
TAT Tyr Ala	GCG Ala	TGAGAGAGTC	CACCTCCAGT	GTAGAGACAT	AACTGACTTT	TGTAAATGCT										2022
GCTGAGGAAC	AAATGAAGGT	CATCCGGGAG	AGAAATGAAG	AAATCTCTGG	AGCCAGCTTC											2082
TAGAGGTAGG	AAAGAGAAGA	TGTTCTTATT	CAGATAATGC	AAGAGAAGCA	ATTCGTCAGT											2142
TTCACTGGGT	ATCTGCAAGG	CTTATTGATT	ATTCTAATCT	AATAAGACAA	GTTTGTGGAA											2202
ATGCAAGATG	AATACAAGCC	TTGGGTCCAT	GTTTACTCTC	TTCTATTTGG	AGAATAAGAT											2262
GGATGCTTAT	TGAAGCCCAG	ACATTCTTGC	AGCTTGGACT	GCATTTTAAG	CCCTGCAGGC											2322
TTCTGCCATA	TCCATGAGAA	GATTCTACAC	TAGCGTCCTG	TTGGGAATTA	TGCCCTGGAA											2382
TTCTGCCTGA	ATTGACCTAC	GCATCTCCTC	CTCCTTGGAC	ATTCTTTTGT	CTTCATTTGG											2442
TGCTTTTGGT	TTGCACCTC	TCCGTGATTG	TAGCCCTACC	AGCATGTTAT	AGGGCAAGAC											2502
CTTTGTGCTT	TTGATCATTC	TGGCCCATGA	AAGCAACTTT	GGTCTCCTTT	CCCCTCCTGT											2562
CTTCCCGGTA	TCCCTTGGAG	TCTCACAAGG	TTTACTTTGG	TATGGTTCTC	AGCACAAACC											2622

111

TTTCAAGTAT	GTTGTTTCTT	TGGAAAATGG	ACATACTGTA	TTGTGTTCTC	CTGCATATAT	2682
CATTCCTGGA	GAGAGAAGGG	GAGAAGAATA	CTTTTCTTCA	ACAAATTTTG	GGGGCAGGAG	2742
ATCCCTTCAA	GAGGCTGCAC	CTTAATTTTT	CTTGTCTGTG	TGCAGGTCTT	CATATAAACT	2802
TTACCAGGAA	GAAGGGTGTG	AGTTTGTGTG	TTTTCTGTGT	ATGGGCCTGG	TCAGTGTAAG	2862
GTTTTATCCT	TGATAGTCTA	GTTACTATGA	CCCTCCCCAC	TTTTTTAAAA	CCAGAAAAAG	2922
GTTTGGAATG	TTGGAATGAC	CAAGAGACAA	GTTAACTCGT	GCAAGAGCCA	GTTACCCACC	2982
CACAGGTCCC	CCTACTTCCT	GCCAAGCATT	CCATTGACTG	CCTGTATGGA	ACACATTTGT	3042
CCCAGATCTG	AGCATTCTAG	GCCTGTTTCA	CTCACTCACC	CAGCATATGA	AACTAGTCTT	3102
AACTGTTGAG	CCTTTCCTTT	CATATCCACA	GAAGACACTG	TCTCAAATGT	TGTACCCTTG	3162
CCATTTAGGA	CTGAACCTTC	CTTAGCCCAA	GGGACCCAGT	GACAGTTGTC	TTCCGTTTGT	3222
CAGATGATCA	GTCTCTACTG	ATTATCTTGC	TGCTTAAAGG	CCTGCTCACC	AATCTTTCTT	3282
TCACACCGTG	TGGTCCGTGT	TACTGGTATA	CCCAGTATGT	TCTCACTGAA	GACATGGACT	3342
TTATATGTTT	AAGTGCAGGA	ATTGGAAAGT	TGGACTTGTT	TTCTATGATC	CAAAACAGCC	3402
CTATAAGAAG	GTTGGAAAAG	GAGGAACTAT	ATAGCAGCCT	TTGCTATTTT	CTGCTACCAT	3462
TTCTTTTCCT	CTGAAGCGGC	CATGACATTC	CCTTTGGCAA	CTAACGTAGA	AACTCAACAG	3522
AACATTTTCC	TTTCCTAGAG	TCACCTTTTA	GATGATAATG	GACAACTATA	GACTTGCTCA	3582
TTGTTTCAGAC	TGATTGCCCC	TCACCTGAAT	CCACTCTCTG	TATTCATGCT	CTTGGCAATT	3642
TCTTTGACTT	TCTTTTAAGG	GCAGAAGCAT	TTAGTTAAT	TGTAGATAAA	GAATAGTTTT	3702
CTTCCTCTTC	TCCTTGGGCC	AGTTAATAAT	TGGTCCATGG	CTACACTGCA	ACTTCCGTCC	3762
AGTGCTGTGA	TGCCCATGAC	ACCTGCAAAA	TAAGTTCTGC	CTGGGCATTT	TGTAGATATT	3822
AACAGGTGAA	TTCCCGACTC	TTTTGGTTTG	AATGACAGTT	CTCATTCCTT	CTATGGCTGC	3882
AAGTATGCAT	CAGTGCTTCC	CACTTACCTG	ATTTGTCTGT	CGGTGGCCCC	ATATGGAAAC	3942
CCTGCGTGTC	TGTTGGCATA	ATAGTTTACA	AATGGTTTTT	TCAGTCCTAT	CCAAATTTAT	4002
TGAACCAACA	AAAATAATTA	CTTCTGCCCT	GAGATAAGCA	GATTAAGTTT	GTTCAATTCTC	4062
TGCTTTATTC	TCTCCATGTG	GCAACATTCT	GTCAGCCTCT	TTCATAGTGT	GCAAACATTT	4122
TATCATTCTA	AATGGTGACT	CTCTGCCCTT	GGACCCATTT	ATTATTCACA	GATGGGGAGA	4182
ACCTATCTGC	ATGGACCCTC	ACCATCCTCT	GTGCAGCACA	CACAGTGCAG	GGAGCCAGTG	4242
GCGATGGCGA	TGACTTTCTT	CCCCTG				4268

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

112

113

355					360					365					
Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	Ala	Pro	Val	His	Ala	Gln	His	Ala
370						375					380				
Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	Met	Gln	Pro	Leu	Ala	His	Gly	Ala
385					390					395					400
Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Gln	Leu	Leu	Ser	His	His	His	Ile
				405					410					415	
Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	Gly	Ser	Leu	Ser	Arg	Leu	His	Pro
			420					425					430		
Val	Pro	Val	Pro	Ala	Asp	Trp	Met	Asn	Arg	Met	Glu	Val	Asn	Glu	Thr
			435				440					445			
Gln	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu	Ala	Pro	Ala	Glu	Gly	Thr
	450					455					460				
His	Pro	Gly	Ile	Ala	Pro	Gln	Ser	Arg	Pro	Pro	Glu	Gly	Lys	His	Ile
465					470					475					480
Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile	Val	Thr	Phe	Gln	Leu	Ile
				485					490					495	
Pro	Lys	Gly	Ser	Ile	Ala	Gln	Pro	Ala	Gly	Ala	Pro	Gln	Pro	Gln	Ser
			500					505					510		
Thr	Cys	Pro	Pro	Ala	Val	Ala	Gly	Pro	Leu	Pro	Thr	Met	Tyr	Gln	Ile
		515					520					525			
Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala	Phe	Pro	Thr	Ala	Met	Met
	530					535					540				
Pro	Gln	Gln	Asp	Gly	Gln	Val	Ala	Gln	Thr	Ile	Leu	Pro	Ala	Tyr	His
545					550					555					560
Pro	Phe	Pro	Ala	Ser	Val	Gly	Lys	Tyr	Pro	Thr	Pro	Pro	Ser	Gln	His
				565					570					575	
Ser	Tyr	Ala	Ser	Ser	Asn	Ala	Ala	Glu	Arg	Thr	Pro	Ser	His	Ser	Gly
			580					585					590		
His	Leu	Gln	Gly	Glu	His	Pro	Tyr	Leu	Thr	Pro	Ser	Pro	Glu	Ser	Pro
		595					600					605			
Asp	Gln	Trp	Ser	Ser	Ser	Pro	His	Ser	Ala	Ser	Asp	Trp	Ser	Asp	
	610					615					620				
Val	Thr	Thr	Ser	Pro	Thr	Pro	Gly	Gly	Ala	Gly	Gly	Gly	Gln	Arg	Gly
625					630					635					640
Pro	Gly	Thr	His	Met	Ser	Glu	Pro	Pro	His	Asn	Asn	Met	Gln	Val	Tyr
				645					650					655	

Ala

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

114

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu	Asp	Ile	Asp	Glu	Cys	Asp	Gln	Gly	Ser	Pro	Cys	Glu	His	Asn	Gly
1				5					10					15	
Ile	Cys	Val	Asn	Thr	Pro	Gly	Ser	Tyr	Arg	Cys	Asn	Cys	Ser	Gln	Gly
			20					25					30		
Phe	Thr	Gly	Pro	Arg	Cys	Glu	Thr	Asn	Ile	Asn	Glu	Cys	Glu	Ser	His
		35					40					45			
Pro	Cys	Gln	Asn	Glu	Gly	Ser	Cys	Leu	Asp	Asp	Pro	Gly	Thr	Phe	Arg
	50					55					60				
Cys	Val	Cys	Met	Pro	Gly	Phe	Thr	Gly	Thr	Gln	Cys	Glu			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn	Asp	Val	Asp	Glu	Cys	Ser	Leu	Gly	Ala	Asn	Pro	Cys	Glu	His	Gly
1				5					10					15	
Gly	Arg	Cys	Thr	Asn	Thr	Leu	Gly	Ser	Phe	Gln	Cys	Asn	Cys	Pro	Gln
			20					25					30		
Gly	Tyr	Ala	Gly	Pro	Arg	Cys	Glu	Ile	Asp	Val	Asn	Glu	Cys	Leu	Ser
		35					40					45			
Asn	Pro	Cys	Gln	Asn	Asp	Ser	Thr	Cys	Leu	Asp	Gln	Ile	Gly	Glu	Phe
	50					55					60				
Gln	Cys	Ile	Cys	Met	Pro	Gly	Tyr	Glu	Gly	Leu	Tyr	Cys	Glu		
65					70					75					

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 654 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Pro Pro Gln Gly Glu Ile Glu Ala Asp Cys Met Asp Val Asn Val

1	5	10	15
Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly	20	25	30
Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Ser Ala	35	40	45
Asn Met Ile Ser Asp Phe Ile Gly Gln Gly Ala Gln Leu His Asn Gln	50	55	60
Thr Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ala	65	70	75
Arg Ala Asp Ala Ala Lys Arg Leu Leu Glu Ser Ser Ala Asp Ala Asn	85	90	95
Val Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ala Ala	100	105	110
Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Ala Thr Asp	115	120	125
Leu Asp Ala Arg Met Phe Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala	130	135	140
Arg Leu Ala Val Glu Gly Met Val Glu Glu Leu Ile Asn Ala His Ala	145	150	155
Asp Val Asn Ala Val Asp Glu Phe Gly Lys Ser Ala Leu His Trp Ala	165	170	175
Ala Ala Val Asn Asn Val Asp Ala Ala Ala Val Leu Leu Lys Asn Ser	180	185	190
Ala Asn Lys Asp Met Gln Asn Asn Lys Glu Glu Thr Ser Leu Phe Leu	195	200	205
Ala Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His	210	215	220
Tyr Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp	225	230	235
Ile Ala Gln Glu Arg Met His His Asp Ile Val His Leu Leu Asp Glu	245	250	255
Tyr Asn Leu Val Lys Ser Pro Thr Leu His Asn Gly Pro Leu Gly Ala	260	265	270
Thr Thr Leu Ser Pro Pro Ile Cys Ser Pro Asn Gly Tyr Met Gly Asn	275	280	285
Met Lys Pro Ser Val Gln Ser Lys Lys Ala Arg Lys Pro Ser Ile Lys	290	295	300
Gly Asn Gly Cys Lys Glu Ala Lys Glu Leu Lys Ala Arg Arg Lys Lys	305	310	315
Ser Gln Asp Gly Lys Thr Thr Leu Leu Asp Ser Gly Ser Ser Gly Val	325	330	335
Leu Ser Pro Val Asp Ser Leu Glu Ser Thr His Gly Tyr Leu Ser Asp	340	345	350
Val Ser Ser Pro Pro Leu Met Thr Ser Pro Phe Gln Gln Ser Pro Ser	355	360	365

116

Met Pro Leu Asn His Leu Thr Ser Met Pro Glu Ser Gln Leu Gly Met
370 375 380

Asn His Ile Asn Met Ala Thr Lys Gln Glu Met Ala Ala Gly Ser Asn
385 390 395 400

Arg Met Ala Phe Asp Ala Met Val Pro Arg Leu Thr His Leu Asn Ala
405 410 415

Ser Ser Pro Asn Thr Ile Met Ser Asn Gly Ser Met His Phe Thr Val
420 425 430

Gly Gly Ala Pro Thr Met Asn Ser Gln Cys Asp Trp Leu Ala Arg Leu
435 440 445

Gln Asn Gly Met Val Gln Asn Gln Tyr Asp Pro Ile Arg Asn Gly Ile
450 455 460

Gln Gln Gly Asn Ala Gln Gln Ala Gln Ala Leu Gln His Gly Leu Met
465 470 475 480

Thr Ser Leu His Asn Gly Leu Pro Ala Thr Thr Leu Ser Gln Met Met
485 490 495

Thr Tyr Gln Ala Met Pro Asn Thr Arg Leu Ala Asn Gln Pro His Leu
500 505 510

Met Gln Ala Gln Gln Met Gln Gln Gln Gln Asn Leu Gln Leu His Gln
515 520 525

Ser Met Gln Gln Gln His His Asn Ser Ser Thr Thr Ser Thr His Ile
530 535 540

Asn Ser Pro Phe Cys Ser Ser Asp Ile Ser Gln Thr Asp Leu Gln Gln
545 550 555 560

Met Ser Ser Asn Asn Ile His Ser Val Met Pro Gln Asp Thr Gln Ile
565 570 575

Phe Ala Ala Ser Leu Pro Ser Asn Leu Thr Gln Ser Met Thr Thr Ala
580 585 590

Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro Met Asp
595 600 605

Asn Thr Pro Ser His Gln Leu Gln Val Pro Asp His Pro Phe Leu Thr
610 615 620

Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser
625 630 635 640

Asn Met Ser Asp Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr
645 650

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

117

Thr	Pro	Pro	Gln	Gly	Glu	Val	Asp	Ala	Asp	Cys	Met	Asp	Val	Asn	Val	1	5	10	15
Arg	Gly	Pro	Asp	Gly	Phe	Thr	Pro	Leu	Met	Ile	Ala	Ser	Cys	Ser	Gly	20	25	30	
Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Pro	Ala	35	40	45	
Val	Ile	Ser	Asp	Phe	Ile	Tyr	Gln	Gly	Ala	Ser	Leu	His	Asn	Gln	Thr	50	55	60	
Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His	Leu	Ala	Ala	Arg	Tyr	Ser	Arg	65	70	75	80
Ser	Asp	Ala	Ala	Lys	Arg	Leu	Leu	Glu	Ala	Ser	Ala	Asp	Ala	Asn	Ile	85	90	95	
Gln	Asp	Asn	Met	Gly	Arg	Thr	Pro	Leu	His	Ala	Ala	Val	Ser	Ala	Asp	100	105	110	
Ala	Gln	Gly	Val	Phe	Gln	Ile	Leu	Leu	Arg	Asn	Arg	Ala	Thr	Asp	Leu	115	120	125	
Asp	Ala	Arg	Met	His	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala	Arg	130	135	140	
Leu	Ala	Val	Glu	Gly	Met	Leu	Glu	Asp	Leu	Ile	Asn	Ser	His	Ala	Asp	145	150	155	160
Val	Asn	Ala	Val	Asp	Asp	Leu	Gly	Lys	Ser	Ala	Leu	His	Trp	Ala	Ala	165	170	175	
Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Val	Val	Leu	Leu	Lys	Asn	Gly	Ala	180	185	190	
Asn	Lys	Asp	Met	Gln	Asn	Asn	Lys	Glu	Glu	Thr	Pro	Leu	Phe	Leu	Ala	195	200	205	
Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Thr	Ala	Lys	Val	Leu	Leu	Asp	His	Phe	210	215	220	
Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg	Leu	Pro	Arg	Asp	Ile	225	230	235	240
Ala	Gln	Glu	Arg	Met	His	His	Asp	Ile	Val	Arg	Leu	Leu	Asp	Glu	Tyr	245	250	255	
Asn	Leu	Val	Arg	Ser	Pro	Gln	Leu	His	Gly	Thr	Ala	Leu	Gly	Gly	Thr	260	265	270	
Pro	Thr	Leu	Ser	Pro	Thr	Leu	Cys	Ser	Pro	Asn	Gly	Tyr	Leu	Gly	Asn	275	280	285	
Leu	Lys	Ser	Ala	Thr	Gln	Gly	Lys	Lys	Ala	Arg	Lys	Pro	Ser	Thr	Lys	290	295	300	
Gly	Leu	Ala	Cys	Ser	Ser	Lys	Glu	Ala	Lys	Asp	Leu	Lys	Ala	Arg	Arg	305	310	315	320
Lys	Lys	Ser	Gln	Asp	Gly	Lys	Gly	Cys	Leu	Leu	Asp	Ser	Ser	Ser	Met	325	330	335	
Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Gly	Tyr	Leu	Ser	Asp	340	345	350	
Val	Ala	Ser	Pro	Pro	Leu	Pro	Ser	Pro	Phe	Gln	Gln	Ser	Pro	Ser	Met				

118

355					360					365					
Pro	Leu	Ser	His	Leu	Pro	Gly	Met	Pro	Asp	Thr	His	Leu	Gly	Ile	Ser
370					375					380					
His	Leu	Asn	Val	Ala	Ala	Lys	Pro	Glu	Met	Ala	Ala	Leu	Ala	Gly	Gly
385					390					395					400
Ser	Arg	Leu	Ala	Phe	Glu	Pro	Pro	Pro	Pro	Arg	Leu	Ser	His	Leu	Pro
				405					410					415	
Val	Ala	Ser	Ser	Ala	Ser	Thr	Val	Leu	Ser	Thr	Asn	Gly	Thr	Gly	Ala
				420				425					430		
Met	Asn	Phe	Thr	Val	Gly	Ala	Pro	Ala	Ser	Leu	Asn	Gly	Gln	Cys	Glu
		435					440					445			
Trp	Leu	Pro	Arg	Leu	Gln	Asn	Gly	Met	Val	Pro	Ser	Gln	Tyr	Asn	Pro
	450					455						460			
Leu	Arg	Pro	Gly	Val	Thr	Pro	Gly	Thr	Leu	Ser	Thr	Gln	Ala	Ala	Gly
465						470					475				480
Leu	Gln	His	Gly	Met	Met	Ser	Pro	Ile	His	Ser	Ser	Leu	Ser	Thr	Asn
				485					490					495	
Thr	Leu	Ser	Pro	Ile	Ile	Tyr	Gln	Gly	Leu	Pro	Asn	Thr	Arg	Leu	Ala
			500					505					510		
Thr	Gln	Pro	His	Leu	Val	Gln	Thr	Gln	Gln	Val	Gln	Pro	Gln	Asn	Leu
		515					520					525			
Gln	Ile	Gln	Pro	Gln	Asn	Leu	Gln	Pro	Pro	Ser	Gln	Pro	His	Leu	Ser
	530					535					540				
Val	Ser	Ser	Ala	Ala	Asn	Gly	His	Leu	Gly	Arg	Ser	Phe	Leu	Ser	Gly
545						550					555				560
Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro	Leu	Gly	Pro	Ser	Ser	Leu	Pro
				565					570					575	
Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser	Gln	Ala	Leu	Pro	Thr	Ser	Leu
			580					585					590		
Pro	Ser	Ser	Met	Val	Pro	Pro	Met	Thr	Thr	Thr	Gln	Phe	Leu	Thr	Pro
			595				600					605			
Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro	Val	Asp	Asn	Thr	Pro	Ser	
	610					615					620				
His	Gln	Leu	Gln	Val	Pro	Glu	His	Pro	Phe	Leu	Thr	Pro	Ser	Pro	Glu
625						630					635				640
Ser	Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Arg	His	Ser	Asn	Ile	Ser	Asp
				645					650					655	
Trp	Ser	Glu	Gly	Ile	Ser	Ser	Pro	Pro	Thr						
			660						665						

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

119

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr	Pro	Pro	Gln	Gly	Glu	Val	Asp	Ala	Asp	Cys	Met	Asp	Val	Asn	Val	1	5	10	15
Arg	Gly	Pro	Asp	Gly	Phe	Thr	Pro	Leu	Met	Ile	Ala	Ser	Cys	Ser	Gly	20	25	30	
Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Pro	Ala	35	40	45	
Val	Ile	Ser	Asp	Phe	Ile	Tyr	Gln	Gly	Ala	Ser	Leu	His	Asn	Gln	Thr	50	55	60	
Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His	Leu	Ala	Ala	Arg	Tyr	Ser	Arg	65	70	75	80
Ser	Asp	Ala	Ala	Lys	Arg	Leu	Leu	Glu	Ala	Ser	Ala	Asp	Ala	Asn	Ile	85	90	95	
Gln	Asp	Asn	Met	Gly	Arg	Thr	Pro	Leu	His	Ala	Ala	Val	Ser	Ala	Asp	100	105	110	
Ala	Gln	Gly	Val	Phe	Gln	Ile	Leu	Ile	Arg	Asn	Arg	Ala	Thr	Asp	Leu	115	120	125	
Asp	Ala	Arg	Met	His	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala	Arg	130	135	140	
Leu	Ala	Val	Glu	Gly	Met	Leu	Glu	Asp	Leu	Ile	Asn	Ser	His	Ala	Asp	145	150	155	160
Val	Asn	Ala	Val	Asp	Asp	Leu	Gly	Lys	Ser	Ala	Leu	His	Trp	Ala	Ala	165	170	175	
Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Val	Val	Leu	Leu	Lys	Asn	Gly	Ala	180	185	190	
Asn	Lys	Asp	Met	Gln	Asn	Asn	Arg	Glu	Glu	Thr	Pro	Leu	Phe	Leu	Ala	195	200	205	
Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Thr	Ala	Lys	Val	Leu	Leu	Asp	His	Phe	210	215	220	
Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg	Leu	Pro	Arg	Asp	Ile	225	230	235	240
Ala	Gln	Glu	Arg	Met	His	His	Asp	Ile	Val	Arg	Leu	Leu	Asp	Glu	Tyr	245	250	255	
Asn	Leu	Val	Arg	Ser	Pro	Gln	Leu	His	Gly	Ala	Pro	Leu	Gly	Gly	Thr	260	265	270	
Pro	Thr	Leu	Ser	Pro	Pro	Leu	Cys	Ser	Pro	Asn	Gly	Tyr	Leu	Gly	Ser	275	280	285	
Leu	Lys	Pro	Gly	Val	Gln	Gly	Lys	Lys	Val	Arg	Lys	Pro	Ser	Ser	Lys	290	295	300	
Gly	Leu	Ala	Cys	Gly	Ser	Lys	Glu	Ala	Lys	Asp	Leu	Lys	Ala	Arg	Arg	305	310	315	320
Lys	Lys	Ser	Gln	Asp	Gly	Lys	Gly	Cys	Leu	Leu	Asp	Ser	Ser	Gly	Met				

(20)

325										330					335				
Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Gly	Tyr	Leu	Ser	Asp				
			340					345					350						
Val	Ala	Ser	Pro	Pro	Leu	Leu	Pro	Ser	Pro	Phe	Gln	Gln	Ser	Pro	Ser				
		355					360					365							
Val	Pro	Leu	Asn	His	Leu	Pro	Gly	Met	Pro	Asp	Thr	His	Leu	Gly	Ile				
	370					375					380								
Gly	His	Leu	Asn	Val	Ala	Ala	Lys	Pro	Glu	Met	Ala	Ala	Leu	Gly	Gly				
385					390					395					400				
Gly	Gly	Arg	Leu	Ala	Phe	Glu	Thr	Gly	Pro	Pro	Arg	Leu	Ser	His	Leu				
				405					410					415					
Pro	Val	Ala	Ser	Gly	Thr	Ser	Thr	Val	Leu	Gly	Ser	Ser	Ser	Gly	Gly				
			420					425					430						
Ala	Leu	Asn	Phe	Thr	Val	Gly	Gly	Ser	Thr	Ser	Leu	Asn	Gly	Gln	Cys				
		435					440					445							
Glu	Trp	Leu	Ser	Arg	Leu	Gln	Ser	Gly	Met	Val	Pro	Asn	Gln	Tyr	Asn				
	450					455					460								
Pro	Leu	Arg	Gly	Ser	Val	Ala	Pro	Gly	Pro	Leu	Ser	Thr	Gln	Ala	Pro				
465					470					475					480				
Ser	Leu	Gln	His	Gly	Met	Val	Gly	Pro	Leu	His	Ser	Ser	Leu	Ala	Ala				
				485					490					495					
Ser	Ala	Leu	Ser	Gln	Met	Met	Ser	Tyr	Gln	Gly	Leu	Pro	Ser	Thr	Arg				
			500					505					510						
Leu	Ala	Thr	Gln	Pro	His	Leu	Val	Gln	Thr	Gln	Gln	Val	Gln	Pro	Gln				
		515					520					525							
Asn	Leu	Gln	Met	Gln	Gln	Gln	Asn	Leu	Gln	Pro	Ala	Asn	Ile	Gln	Gln				
	530					535					540								
Gln	Gln	Ser	Leu	Gln	Pro	Pro	Pro	Pro	Pro	Pro	Gln	Pro	His	Leu	Gly				
545					550					555					560				
Val	Ser	Ser	Ala	Ala	Ser	Gly	His	Leu	Gly	Arg	Ser	Phe	Leu	Ser	Gly				
				565					570					575					
Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro	Leu	Gly	Pro	Ser	Ser	Leu	Ala				
			580					585					590						
Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser	Pro	Ala	Leu	Pro	Thr	Ser	Leu				
		595					600					605							
Pro	Ser	Ser	Leu	Val	Pro	Pro	Val	Thr	Ala	Ala	Gln	Phe	Leu	Thr	Pro				
	610					615					620								
Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro	Val	Glu	Asn	Thr	Pro	Ser	His				
625					630					635					640				
Gln	Leu	Gln	Val	Pro	Glu	His	Pro	Phe	Leu	Thr	Pro	Ser	Pro	Glu	Ser				
				645					650					655					
Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser	Asn	Val	Ser	Asp	Trp				
			660					665					670						
Ser	Glu	Gly	Val	Ser	Ser	Pro	Pro	Thr											
		675					680												

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Pro	Ala	Leu	Arg	Pro	Ala	Leu	Leu	Trp	Ala	Leu	Leu	Ala	Leu	Trp	1	5	10	15
Leu	Cys	Cys	Ala	Ala	Pro	Ala	His	Ala	Leu	Gln	Cys	Arg	Asp	Gly	Tyr	20	25	30	
Glu	Pro	Cys	Val	Asn	Glu	Gly	Met	Cys	Val	Thr	Tyr	His	Asn	Gly	Thr	35	40	45	
Gly	Tyr	Cys	Lys	Cys	Pro	Glu	Gly	Phe	Leu	Gly	Glu	Tyr	Cys	Gln	His	50	55	60	
Arg	Asp	Pro	Cys	Glu	Lys	Asn	Arg	Cys	Gln	Asn	Gly	Gly	Thr	Cys	Val	65	70	75	80
Ala	Gln	Ala	Met	Leu	Gly	Lys	Ala	Thr	Cys	Arg	Cys	Ala	Ser	Gly	Phe	85	90	95	
Thr	Gly	Glu	Asp	Cys	Gln	Tyr	Ser	Thr	Ser	His	Pro	Cys	Phe	Val	Ser	100	105	110	
Arg	Pro	Cys	Leu	Asn	Gly	Gly	Thr	Cys	His	Met	Leu	Ser	Arg	Asp	Thr	115	120	125	
Tyr	Glu	Cys	Thr	Cys	Gln	Val	Gly	Phe	Thr	Gly	Lys	Glu	Cys	Gln	Trp	130	135	140	
Thr	Asp	Ala	Cys	Leu	Ser	His	Pro	Cys	Ala	Asn	Gly	Ser	Thr	Cys	Thr	145	150	155	160
Thr	Val	Ala	Asn	Gln	Phe	Ser	Cys	Lys	Cys	Leu	Thr	Gly	Phe	Thr	Gly	165	170	175	
Gln	Lys	Cys	Glu	Thr	Asp	Val	Asn	Glu	Cys	Asp	Ile	Pro	Gly	His	Cys	180	185	190	
Gln	His	Gly	Gly	Thr	Cys	Leu	Asn	Leu	Pro	Gly	Ser	Tyr	Gln	Cys	Gln	195	200	205	
Cys	Pro	Gln	Gly	Phe	Thr	Gly	Gln	Tyr	Cys	Asp	Ser	Leu	Tyr	Val	Pro	210	215	220	
Cys	Ala	Pro	Ser	Pro	Cys	Val	Asn	Gly	Gly	Thr	Cys	Arg	Gln	Thr	Gly	225	230	235	240
Asp	Phe	Thr	Phe	Glu	Cys	Asn	Cys	Leu	Pro	Gly	Phe	Glu	Gly	Ser	Thr	245	250	255	
Cys	Glu	Arg	Asn	Ile	Asp	Asp	Cys	Pro	Asn	His	Arg	Cys	Gln	Asn	Gly	260	265	270	
Gly	Val	Cys	Val	Asp	Gly	Val	Asn	Thr	Tyr	Asn	Cys	Arg	Cys	Pro	Pro	275	280	285	

122

Gln	Trp	Thr	Gly	Gln	Phe	Cys	Thr	Glu	Asp	Val	Asp	Glu	Cys	Leu	Leu
290						295					300				
Gln	Pro	Asn	Ala	Cys	Gln	Asn	Gly	Gly	Thr	Cys	Ala	Asn	Arg	Asn	Gly
305					310					315					320
Gly	Tyr	Gly	Cys	Val	Cys	Val	Asn	Gly	Trp	Ser	Gly	Asp	Asp	Cys	Ser
				325					330					335	
Glu	Asn	Ile	Asp	Asp	Cys	Ala	Phe	Ala	Ser	Cys	Thr	Pro	Gly	Ser	Thr
			340					345					350		
Cys	Ile	Asp	Arg	Val	Ala	Ser	Phe	Ser	Cys	Met	Cys	Pro	Glu	Gly	Lys
		355					360					365			
Ala	Gly	Leu	Leu	Cys	His	Leu	Asp	Asp	Ala	Cys	Ile	Ser	Asn	Pro	Cys
	370					375					380				
His	Lys	Gly	Ala	Leu	Cys	Asp	Thr	Asn	Pro	Leu	Asn	Gly	Gln	Tyr	Ile
385					390					395					400
Cys	Thr	Cys	Pro	Gln	Gly	Tyr	Lys	Gly	Ala	Asp	Cys	Thr	Glu	Asp	Val
				405					410					415	
Asp	Glu	Cys	Ala	Met	Ala	Asn	Ser	Asn	Pro	Cys	Glu	His	Ala	Gly	Lys
			420					425					430		
Cys	Val	Asn	Thr	Asp	Gly	Ala	Phe	His	Cys	Glu	Cys	Leu	Lys	Gly	Tyr
		435					440					445			
Ala	Gly	Pro	Arg	Cys	Glu	Met	Asp	Ile	Asn	Glu	Cys	His	Ser	Asp	Pro
	450					455					460				
Cys	Gln	Asn	Asp	Ala	Thr	Cys	Leu	Asp	Lys	Ile	Gly	Gly	Phe	Thr	Cys
465					470					475					480
Leu	Cys	Met	Pro	Gly	Phe	Lys	Gly	Val	His	Cys	Glu	Leu	Glu	Ile	Asn
				485					490					495	
Glu	Cys	Gln	Ser	Asn	Pro	Cys	Val	Asn	Asn	Gly	Gln	Cys	Val	Asp	Lys
			500					505					510		
Val	Asn	Arg	Phe	Gln	Cys	Leu	Cys	Pro	Pro	Gly	Phe	Thr	Gly	Pro	Val
		515					520					525			
Cys	Gln	Ile	Asp	Ile	Asp	Asp	Cys	Ser	Ser	Thr	Pro	Cys	Leu	Asn	Gly
	530					535					540				
Ala	Lys	Cys	Ile	Asp	His	Pro	Asn	Gly	Tyr	Glu	Cys	Gln	Cys	Ala	Thr
545					550					555					560
Gly	Phe	Thr	Gly	Val	Leu	Cys	Glu	Glu	Asn	Ile	Asp	Asn	Cys	Asp	Pro
				565					570					575	
Asp	Pro	Cys	His	His	Gly	Gln	Cys	Gln	Asp	Gly	Ile	Asp	Ser	Tyr	Thr
			580					585					590		
Cys	Ile	Cys	Asn	Pro	Gly	Tyr	Met	Gly	Ala	Ile	Cys	Ser	Asp	Gln	Ile
		595					600					605			
Asp	Glu	Cys	Tyr	Ser	Ser	Pro	Cys	Leu	Asn	Asp	Gly	Arg	Cys	Ile	Asp
	610					615					620				
Leu	Val	Asn	Gly	Tyr	Gln	Cys	Asn	Cys	Gln	Pro	Gly	Thr	Ser	Gly	Val
625					630					635					640
Asn	Cys	Glu	Ile	Asn	Phe	Asp	Asp	Cys	Ala	Ser	Asn	Pro	Cys	Ile	His

645					650					655					
Gly	Ile	Cys	Met	Asp	Gly	Ile	Asn	Arg	Tyr	Ser	Cys	Val	Cys	Ser	Pro
			660					665					670		
Gly	Phe	Thr	Gly	Gln	Arg	Cys	Asn	Ile	Asp	Ile	Asp	Glu	Cys	Ala	Ser
		675					680					685			
Asn	Pro	Cys	Arg	Lys	Gly	Ala	Thr	Cys	Ile	Asn	Gly	Val	Asn	Gly	Phe
	690					695					700				
Arg	Cys	Ile	Cys	Pro	Glu	Gly	Pro	His	His	Pro	Ser	Cys	Tyr	Ser	Gln
705					710					715					720
Val	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Ile	His	Gly	Asn	Cys	Thr	Gly
				725					730					735	
Gly	Leu	Ser	Gly	Tyr	Lys	Cys	Leu	Cys	Asp	Ala	Gly	Trp	Val	Gly	Ile
			740					745					750		
Asn	Cys	Glu	Val	Asp	Lys	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Gln	Asn
		755					760					765			
Gly	Gly	Thr	Cys	Asp	Asn	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Thr	Cys	Lys
	770					775					780				
Lys	Gly	Phe	Lys	Gly	Tyr	Asn	Cys	Gln	Val	Asn	Ile	Asp	Glu	Cys	Ala
785					790					795					800
Ser	Asn	Pro	Cys	Leu	Asn	Gln	Gly	Thr	Cys	Phe	Asp	Asp	Ile	Ser	Gly
				805					810					815	
Tyr	Thr	Cys	His	Cys	Val	Leu	Pro	Tyr	Thr	Gly	Lys	Asn	Cys	Gln	Thr
			820					825					830		
Val	Leu	Ala	Pro	Cys	Ser	Pro	Asn	Pro	Cys	Glu	Asn	Ala	Ala	Val	Cys
		835					840					845			
Lys	Glu	Ser	Pro	Asn	Phe	Glu	Ser	Tyr	Thr	Cys	Leu	Cys	Ala	Pro	Gly
	850					855					860				
Trp	Gln	Gly	Gln	Arg	Cys	Thr	Ile	Asp	Ile	Asp	Glu	Cys	Ile	Ser	Lys
865					870					875					880
Pro	Cys	Met	Asn	His	Gly	Leu	Cys	His	Asn	Thr	Gln	Gly	Ser	Tyr	Met
				885					890					895	
Cys	Glu	Cys	Pro	Pro	Gly	Phe	Ser	Gly	Met	Asp	Cys	Glu	Glu	Asp	Ile
			900					905					910		
Asp	Asp	Cys	Leu	Ala	Asn	Pro	Cys	Gln	Asn	Gly	Gly	Ser	Cys	Met	Asp
		915					920					925			
Gly	Val	Asn	Thr	Phe	Ser	Cys	Leu	Cys	Leu	Pro	Gly	Phe	Thr	Gly	Asp
	930					935					940				
Lys	Cys	Gln	Thr	Asp	Met	Asn	Glu	Cys	Leu	Ser	Glu	Pro	Cys	Lys	Asn
945					950					955					960
Gly	Gly	Thr	Cys	Ser	Asp	Tyr	Val	Asn	Ser	Tyr	Thr	Cys	Lys	Cys	Gln
				965					970					975	
Ala	Gly	Phe	Asp	Gly	Val	His	Cys	Glu	Asn	Asn	Ile	Asn	Glu	Cys	Thr
			980					985					990		
Glu	Ser	Ser	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Val	Asp	Gly	Ile	Asn	Ser
		995					1000					1005			

Phe Ser Cys Leu Cys Pro Val Gly Phe Thr Gly Ser Phe Cys Leu His
1010 1015 1020

Glu Ile Asn Glu Cys Ser Ser His Pro Cys Leu Asn Glu Gly Thr Cys
1025 1030 1035 1040

Val Asp Gly Leu Gly Thr Tyr Arg Cys Ser Cys Pro Leu Gly Tyr Thr
1045 1050 1055

Gly Lys Asn Cys Gln Thr Leu Val Asn Leu Cys Ser Arg Ser Pro Cys
1060 1065 1070

Lys Asn Lys Gly Thr Cys Val Gln Lys Lys Ala Glu Ser Gln Cys Leu
1075 1080 1085

Cys Pro Ser Gly Trp Ala Gly Ala Tyr Cys Asp Val Pro Asn Val Ser
1090 1095 1100

Cys Asp Ile Ala Ala Ser Arg Arg Gly Val Leu Val Glu His Leu Cys
1105 1110 1115 1120

Gln His Ser Gly Val Cys Ile Asn Ala Gly Asn Thr His Tyr Cys Gln
1125 1130 1135

Cys Pro Leu Gly Tyr Thr Gly Ser Tyr Cys Glu Glu Gln Leu Asp Glu
1140 1145 1150

Cys Ala Ser Asn Pro Cys Gln His Gly Ala Thr Cys Ser Asp Phe Ile
1155 1160 1165

Gly Gly Tyr Arg Cys Glu Cys Val Pro Gly Tyr Gln Gly Val Asn Cys
1170 1175 1180

Glu Tyr Glu Val Asp Glu Cys Gln Asn Gln Pro Cys Gln Asn Gly Gly
1185 1190 1195 1200

Thr Cys Ile Asp Leu Val Asn His Phe Lys Cys Ser Cys Pro Pro Gly
1205 1210 1215

Thr Arg Gly Leu Leu Cys Glu Glu Asn Ile Asp Asp Cys Ala Arg Gly
1220 1225 1230

Pro His Cys Leu Asn Gly Gly Gln Cys Met Asp Arg Ile Gly Gly Tyr
1235 1240 1245

Ser Cys Arg Cys Leu Pro Gly Phe Ala Gly Glu Arg Cys Glu Gly Asp
1250 1255 1260

Ile Asn Glu Cys Leu Ser Asn Pro Cys Ser Ser Glu Gly Ser Leu Asp
1265 1270 1275 1280

Cys Ile Gln Leu Thr Asn Asp Tyr Leu Cys Val Cys Arg Ser Ala Phe
1285 1290 1295

Thr Gly Arg His Cys Glu Thr Phe Val Asp Val Cys Pro Gln Met Pro
1300 1305 1310

Cys Leu Asn Gly Gly Thr Cys Ala Val Ala Ser Asn Met Pro Asp Gly
1315 1320 1325

Phe Ile Cys Arg Cys Pro Pro Gly Phe Ser Gly Ala Arg Cys Gln Ser
1330 1335 1340

Ser Cys Gly Gln Val Lys Cys Arg Lys Gly Glu Gln Cys Val His Thr
1345 1350 1355 1360

Ala Ser Gly Pro Arg Cys Phe Cys Pro Ser Pro Arg Asp Cys Glu Ser

125

1365	1370	1375
Gly Cys Ala Ser Ser Pro Cys Gln His Gly Gly Ser Cys His Pro Gln 1380	1385	1390
Arg Gln Pro Pro Tyr Tyr Ser Cys Gln Cys Ala Pro Pro Phe Ser Gly 1395	1400	1405
Ser Arg Cys Glu Leu Tyr Thr Ala Pro Pro Ser Thr Pro Pro Ala Thr 1410	1415	1420
Cys Leu Ser Gln Tyr Cys Ala Asp Lys Ala Arg Asp Gly Val Cys Asp 1425	1430	1435
Glu Ala Cys Asn Ser His Ala Cys Gln Trp Asp Gly Gly Asp Cys Ser 1445	1450	1455
Leu Thr Met Glu Asn Pro Trp Ala Asn Cys Ser Ser Pro Leu Pro Cys 1460	1465	1470
Trp Asp Tyr Ile Asn Asn Gln Cys Asp Glu Leu Cys Asn Thr Val Glu 1475	1480	1485
Cys Leu Phe Asp Asn Phe Glu Cys Gln Gly Asn Ser Lys Thr Cys Lys 1490	1495	1500
Tyr Asp Lys Tyr Cys Ala Asp His Phe Lys Asp Asn His Cys Asn Gln 1505	1510	1515
Gly Cys Asn Ser Glu Glu Cys Gly Trp Asp Gly Leu Asp Cys Ala Ala 1525	1530	1535
Asp Gln Pro Glu Asn Leu Ala Glu Gly Thr Leu Val Ile Val Val Leu 1540	1545	1550
Met Pro Pro Glu Gln Leu Leu Gln Asp Ala Arg Ser Phe Leu Arg Ala 1555	1560	1565
Leu Gly Thr Leu Leu His Thr Asn Leu Arg Ile Lys Arg Asp Ser Gln 1570	1575	1580
Gly Glu Leu Met Val Tyr Pro Tyr Tyr Gly Glu Lys Ser Ala Ala Met 1585	1590	1595
Lys Lys Gln Arg Met Thr Arg Arg Ser Leu Pro Gly Glu Gln Glu Gln 1605	1610	1615
Glu Val Ala Gly Ser Lys Val Phe Leu Glu Ile Asp Asn Arg Gln Cys 1620	1625	1630
Val Gln Asp Ser Asp His Cys Phe Lys Asn Thr Asp Ala Ala Ala Ala 1635	1640	1645
Leu Leu Ala Ser His Ala Ile Gln Gly Thr Leu Ser Tyr Pro Leu Val 1650	1655	1660
Ser Val Val Ser Glu Ser Leu Thr Pro Glu Arg Thr Gln Leu Leu Tyr 1665	1670	1675
Leu Leu Ala Val Ala Val Val Ile Ile Leu Phe Ile Ile Leu Leu Gly 1685	1690	1695
Val Ile Met Ala Lys Arg Lys Arg Lys His Gly Ser Leu Trp Leu Pro 1700	1705	1710
Glu Gly Phe Thr Leu Arg Arg Asp Ala Ser Asn His Lys Arg Arg Glu 1715	1720	1725

126

Pro Val Gly Gln Asp Ala Val Gly Leu Lys Asn Leu Ser Val Gln Val
1730 1735 1740

Ser Glu Ala Asn Leu Ile Gly Thr Gly Thr Ser Glu His Trp Val Asp
1745 1750 1755 1760

Asp Glu Gly Pro Gln Pro Lys Lys Val Lys Ala Glu Asp Glu Ala Leu
1765 1770 1775

Leu Ser Glu Glu Asp Asp Pro Ile Asp Arg Arg Pro Trp Thr Gln Gln
1780 1785 1790

His Leu Glu Ala Ala Asp Ile Arg Arg Thr Pro Ser Leu Ala Leu Thr
1795 1800 1805

Pro Pro Gln Ala Glu Gln Glu Val Asp Val Leu Asp Val Asn Val Arg
1810 1815 1820

Gly Pro Asp Gly Cys Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly
1825 1830 1835 1840

Ser Ser Asp Leu Ser Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala
1845 1850 1855

Asn Ile Ile Thr Asp Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln
1860 1865 1870

Thr Asp Arg Thr Gly Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser
1875 1880 1885

Arg Ala Asp Ala Ala Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn
1890 1895 1900

Ala Gln Asp Asn Met Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala
1905 1910 1915 1920

Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp
1925 1930 1935

Leu Asp Ala Arg Met Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala
1940 1945 1950

Arg Leu Ala Val Glu Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala
1955 1960 1965

Asp Val Asn Ala Val Asp Asp His Gly Lys Ser Ala Leu His Trp Ala
1970 1975 1980

Ala Ala Val Asn Asn Val Glu Ala Thr Leu Leu Leu Lys Asn Gly
1985 1990 1995 2000

Ala Asn Arg Asp Met Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu
2005 2010 2015

Ala Ala Arg Glu Gly Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His
2020 2025 2030

Phe Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp
2035 2040 2045

Val Ala Arg Asp Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu
2050 2055 2060

Tyr Asn Val Thr Pro Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu
2065 2070 2075 2080

Ser Pro Val Ile Cys Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His

2085					2090					2095					
Thr	Pro	Met	Gly	Lys	Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	Thr	Met
			2100					2105					2110		
Pro	Thr	Ser	Leu	Pro	Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	Lys	Gly
			2115				2120					2125			
Ser	Arg	Arg	Lys	Lys	Ser	Leu	Ser	Glu	Lys	Val	Gln	Leu	Ser	Glu	Ser
			2130				2135					2140			
Ser	Val	Thr	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Thr	Tyr
			2145				2150					2155			2160
Val	Ser	Asp	Thr	Thr	Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	Ile	Leu
				2165					2170					2175	
Gln	Ala	Ser	Pro	Asn	Pro	Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	Ala	Pro
				2180				2185					2190		
Val	His	Ala	Gln	His	Ala	Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	Met	Gln
			2195				2200					2205			
Pro	Leu	Ala	His	Gly	Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Gln	Leu
			2210				2215					2220			
Leu	Ser	His	His	His	Ile	Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	Gly	Ser
				2225			2230					2235			2240
Leu	Ser	Arg	Leu	His	Pro	Val	Pro	Val	Pro	Ala	Asp	Trp	Met	Asn	Arg
				2245					2250					2255	
Met	Glu	Val	Asn	Glu	Thr	Gln	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu
				2260				2265					2270		
Ala	Pro	Ala	Glu	Gly	Thr	His	Pro	Gly	Ile	Ala	Pro	Gln	Ser	Arg	Pro
				2275				2280					2285		
Pro	Glu	Gly	Lys	His	Ile	Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile
				2290				2295				2300			
Val	Thr	Phe	Gln	Leu	Ile	Pro	Lys	Gly	Ser	Ile	Ala	Gln	Pro	Ala	Gly
				2305				2310				2315			2320
Ala	Pro	Gln	Pro	Gln	Ser	Thr	Cys	Pro	Pro	Ala	Val	Ala	Gly	Pro	Leu
				2325					2330					2335	
Pro	Thr	Met	Tyr	Gln	Ile	Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala
				2340				2345					2350		
Phe	Pro	Thr	Ala	Met	Met	Pro	Gln	Gln	Asp	Gly	Gln	Val	Ala	Gln	Thr
				2355				2360				2365			
Ile	Leu	Pro	Ala	Tyr	His	Pro	Phe	Pro	Ala	Ser	Val	Gly	Lys	Tyr	Pro
				2370				2375				2380			
Thr	Pro	Pro	Ser	Gln	His	Ser	Tyr	Ala	Ser	Ser	Asn	Ala	Ala	Glu	Arg
				2385				2390				2395			2400
Thr	Pro	Ser	His	Ser	Gly	His	Leu	Gln	Gly	Glu	His	Pro	Tyr	Leu	Thr
				2405					2410					2415	
Pro	Ser	Pro	Glu	Ser	Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser
				2420				2425					2430		
Ala	Ser	Asp	Trp	Ser	Asp	Val	Thr	Thr	Ser	Pro	Thr	Pro	Gly	Gly	Ala
				2435				2440					2445		

Gly Gly Gly Gln Arg Gly Pro Gly Thr His Met Ser Glu Pro Pro His
2450 2455 2460

Asn Asn Met Gln Val Tyr Ala
2465 2470

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2556 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Pro	Pro	Leu	Leu	Ala	Pro	Leu	Leu	Cys	Leu	Ala	Leu	Leu	Pro	Ala	1	5	10	15
Leu	Ala	Ala	Arg	Gly	Pro	Arg	Cys	Ser	Gln	Pro	Gly	Glu	Thr	Cys	Leu	20	25	30	
Asn	Gly	Gly	Lys	Cys	Glu	Ala	Ala	Asn	Gly	Thr	Glu	Ala	Cys	Val	Cys	35	40	45	
Gly	Gly	Ala	Phe	Val	Gly	Pro	Arg	Cys	Gln	Asp	Pro	Asn	Pro	Cys	Leu	50	55	60	
Ser	Thr	Pro	Cys	Lys	Asn	Ala	Gly	Thr	Cys	His	Val	Val	Asp	Arg	Arg	65	70	75	80
Gly	Val	Ala	Asp	Tyr	Ala	Cys	Ser	Cys	Ala	Leu	Gly	Phe	Ser	Gly	Pro	85	90	95	
Leu	Cys	Leu	Thr	Pro	Leu	Asp	Asn	Ala	Cys	Leu	Thr	Asn	Pro	Cys	Arg	100	105	110	
Asn	Gly	Gly	Thr	Cys	Asp	Leu	Leu	Thr	Leu	Thr	Glu	Tyr	Lys	Cys	Arg	115	120	125	
Cys	Pro	Pro	Gly	Trp	Ser	Gly	Lys	Ser	Cys	Gln	Gln	Ala	Asp	Pro	Cys	130	135	140	
Ala	Ser	Asn	Pro	Cys	Ala	Asn	Gly	Gly	Gln	Cys	Leu	Pro	Phe	Glu	Ala	145	150	155	160
Ser	Tyr	Ile	Cys	His	Cys	Pro	Pro	Ser	Phe	His	Gly	Pro	Thr	Cys	Arg	165	170	175	
Gln	Asp	Val	Asn	Glu	Cys	Gly	Gln	Lys	Pro	Arg	Leu	Cys	Arg	His	Gly	180	185	190	
Gly	Thr	Cys	His	Asn	Glu	Val	Gly	Ser	Tyr	Arg	Cys	Val	Cys	Arg	Ala	195	200	205	
Thr	His	Thr	Gly	Pro	Asn	Cys	Glu	Arg	Pro	Tyr	Val	Pro	Cys	Ser	Pro	210	215	220	
Ser	Pro	Cys	Gln	Asn	Gly	Gly	Thr	Cys	Arg	Pro	Thr	Gly	Asp	Val	Thr	225	230	235	240
His	Glu	Cys	Ala	Cys	Leu	Pro	Gly	Phe	Thr	Gly	Gln	Asn	Cys	Glu	Glu	245	250	255	

Asn	Ile	Asp	Asp	Cys	Pro	Gly	Asn	Asn	Cys	Lys	Asn	Gly	Gly	Ala	Cys	
			260					265					270			
Val	Asp	Gly	Val	Asn	Thr	Tyr	Asn	Cys	Pro	Cys	Pro	Pro	Glu	Trp	Thr	
		275					280					285				
Gly	Gln	Tyr	Cys	Thr	Glu	Asp	Val	Asp	Glu	Cys	Gln	Leu	Met	Pro	Asn	
	290					295					300					
Ala	Cys	Gln	Asn	Gly	Gly	Thr	Cys	His	Asn	Thr	His	Gly	Gly	Tyr	Asn	
305					310					315					320	
Cys	Val	Cys	Val	Asn	Gly	Trp	Thr	Gly	Glu	Asp	Cys	Ser	Glu	Asn	Ile	
				325					330					335		
Asp	Asp	Cys	Ala	Ser	Ala	Ala	Cys	Phe	His	Gly	Ala	Thr	Cys	His	Asp	
			340					345					350			
Arg	Val	Ala	Ser	Phe	Tyr	Cys	Glu	Cys	Pro	His	Gly	Arg	Thr	Gly	Leu	
		355					360					365				
Leu	Cys	His	Leu	Asn	Asp	Ala	Cys	Ile	Ser	Asn	Pro	Cys	Asn	Glu	Gly	
	370					375					380					
Ser	Asn	Cys	Asp	Thr	Asn	Pro	Val	Asn	Gly	Lys	Ala	Ile	Cys	Thr	Cys	
385					390					395					400	
Pro	Ser	Gly	Tyr	Thr	Gly	Pro	Ala	Cys	Ser	Gln	Asp	Val	Asp	Glu	Cys	
				405					410					415		
Ser	Leu	Gly	Ala	Asn	Pro	Cys	Glu	His	Ala	Gly	Lys	Cys	Ile	Asn	Thr	
			420					425					430			
Leu	Gly	Ser	Phe	Glu	Cys	Gln	Cys	Leu	Gln	Gly	Tyr	Thr	Gly	Pro	Arg	
		435					440					445				
Cys	Glu	Ile	Asp	Val	Asn	Glu	Cys	Val	Ser	Asn	Pro	Cys	Gln	Asn	Asp	
	450					455					460					
Ala	Thr	Cys	Leu	Asp	Gln	Ile	Gly	Glu	Phe	Gln	Cys	Met	Cys	Met	Pro	
465					470					475					480	
Gly	Tyr	Glu	Gly	Val	His	Cys	Glu	Val	Asn	Thr	Asp	Glu	Cys	Ala	Ser	
				485					490					495		
Ser	Pro	Cys	Leu	His	Asn	Gly	Arg	Cys	Leu	Asp	Lys	Ile	Asn	Glu	Phe	
			500					505					510			
Gln	Cys	Glu	Cys	Pro	Thr	Gly	Phe	Thr	Gly	His	Leu	Cys	Gln	Tyr	Asp	
		515					520					525				
Val	Asp	Glu	Cys	Ala	Ser	Thr	Pro	Cys	Lys	Asn	Gly	Ala	Lys	Cys	Leu	
	530					535					540					
Asp	Gly	Pro	Asn	Thr	Tyr	Thr	Cys	Val	Cys	Thr	Glu	Gly	Tyr	Thr	Gly	
545					550					555					560	
Thr	His	Cys	Glu	Val	Asp	Ile	Asp	Glu	Cys	Asp	Pro	Asp	Pro	Cys	His	
				565					570					575		
Tyr	Gly	Ser	Cys	Lys	Asp	Gly	Val	Ala	Thr	Phe	Thr	Cys	Leu	Cys	Arg	
			580					585					590			
Pro	Gly	Tyr	Thr	Gly	His	His	Cys	Glu	Thr	Asn	Ile	Asn	Glu	Cys	Ser	
		595					600					605				
Ser	Gln	Pro	Cys	Arg	Leu	Arg	Gly	Thr	Cys	Gln	Asp	Pro	Asp	Asn	Ala	

610					615					620					
Tyr 625	Leu	Cys	Phe	Cys	Leu 630	Lys	Gly	Thr	Thr	Gly 635	Pro	Asn	Cys	Glu	Ile 640
Asn	Leu	Asp	Asp	Cys 645	Ala	Ser	Ser	Pro	Cys 650	Asp	Ser	Gly	Thr	Cys 655	Leu
Asp	Lys	Ile	Asp 660	Gly	Tyr	Glu	Cys	Ala 665	Cys	Glu	Pro	Gly	Tyr 670	Thr	Gly
Ser	Met	Cys 675	Asn	Ser	Asn	Ile	Asp 680	Glu	Cys	Ala	Gly	Asn 685	Pro	Cys	His
Asn	Gly 690	Gly	Thr	Cys	Glu	Asp 695	Gly	Ile	Asn	Gly	Phe 700	Thr	Cys	Arg	Cys
Pro 705	Glu	Gly	Tyr	His	Asp 710	Pro	Thr	Cys	Leu	Ser 715	Glu	Val	Asn	Glu	Cys 720
Asn	Ser	Asn	Pro	Cys 725	Val	His	Gly	Ala	Cys 730	Arg	Asp	Ser	Leu	Asn 735	Gly
Tyr	Lys	Cys	Asp 740	Cys	Asp	Pro	Gly	Trp 745	Ser	Gly	Thr	Asn	Cys 750	Asp	Ile
Asn	Asn	Asn 755	Glu	Cys	Glu	Ser	Asn 760	Pro	Cys	Val	Asn	Gly 765	Gly	Thr	Cys
Lys	Asp 770	Met	Thr	Ser	Gly	Ile 775	Val	Cys	Thr	Cys	Arg 780	Glu	Gly	Phe	Ser
Gly 785	Pro	Asn	Cys	Gln	Thr 790	Asn	Ile	Asn	Glu	Cys 795	Ala	Ser	Asn	Pro	Cys 800
Leu	Asn	Lys	Gly	Thr 805	Cys	Ile	Asp	Asp	Val 810	Ala	Gly	Tyr	Lys	Cys 815	Asn
Cys	Leu	Leu	Pro 820	Tyr	Thr	Gly	Ala	Thr 825	Cys	Glu	Val	Val	Leu 830	Ala	Pro
Cys	Ala	Pro 835	Ser	Pro	Cys	Arg	Asn 840	Gly	Gly	Glu	Cys	Arg 845	Gln	Ser	Glu
Asp	Tyr 850	Glu	Ser	Phe	Ser	Cys 855	Val	Cys	Pro	Thr	Ala 860	Gly	Ala	Lys	Gly
Gln 865	Thr	Cys	Glu	Val	Asp 870	Ile	Asn	Glu	Cys	Val 875	Leu	Ser	Pro	Cys	Arg 880
His	Gly	Ala	Ser	Cys 885	Gln	Asn	Thr	His	Gly 890	Gly	Tyr	Arg	Cys	His 895	Cys
Gln	Ala	Gly	Tyr 900	Ser	Gly	Arg	Asn 905	Cys	Glu	Thr	Asp	Ile	Asp 910	Asp	Cys
Arg	Pro	Asn 915	Pro	Cys	His	Asn	Gly 920	Gly	Ser	Cys	Thr	Asp 925	Gly	Ile	Asn
Thr 930	Ala	Phe	Cys	Asp	Cys	Leu 935	Pro	Gly	Phe	Arg	Gly 940	Thr	Phe	Cys	Glu
Glu 945	Asp	Ile	Asn	Glu	Cys 950	Ala	Ser	Asp	Pro	Cys 955	Arg	Asn	Gly	Ala	Asn 960
Cys	Thr	Asp	Cys	Val 965	Asp	Ser	Tyr	Thr	Cys 970	Thr	Cys	Pro	Ala	Gly 975	Phe

Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser
980 985 990

Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys
995 1000 1005

Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val Asn
1010 1015 1020

Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln Asp Gly
1025 1030 1035 1040

Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn
1045 1050 1055

Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asn Gly
1060 1065 1070

Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser
1075 1080 1085

Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val
1090 1095 1100

Ala Ala Gln Arg Gln Gly Val Asp Val Ala Arg Leu Cys Gln His Gly
1105 1110 1115 1120

Gly Leu Cys Val Asp Ala Gly Asn Thr His His Cys Arg Cys Gln Ala
1125 1130 1135

Gly Tyr Thr Gly Ser Tyr Cys Glu Asp Leu Val Asp Glu Cys Ser Pro
1140 1145 1150

Ser Pro Cys Gln Asn Gly Ala Thr Cys Thr Asp Tyr Leu Gly Gly Tyr
1155 1160 1165

Ser Cys Lys Cys Val Ala Gly Tyr His Gly Val Asn Cys Ser Glu Glu
1170 1175 1180

Ile Asp Glu Cys Leu Ser His Pro Cys Gln Asn Gly Gly Thr Cys Leu
1185 1190 1195 1200

Asp Leu Pro Asn Thr Tyr Lys Cys Ser Cys Pro Arg Gly Thr Gln Gly
1205 1210 1215

Val His Cys Glu Ile Asn Val Asp Asp Cys Asn Pro Pro Val Asp Pro
1220 1225 1230

Val Ser Arg Ser Pro Lys Cys Phe Asn Asn Gly Thr Cys Val Asp Gln
1235 1240 1245

Val Gly Gly Tyr Ser Cys Thr Cys Pro Pro Gly Phe Val Gly Glu Arg
1250 1255 1260

Cys Glu Gly Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Asp Ala Arg
1265 1270 1275 1280

Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His Cys Glu Cys
1285 1290 1295

Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys
1300 1305 1310

Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn
1315 1320 1325

Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala

132

1330	1335	1340
Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 1345 1350 1355 1360		
Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu 1365 1370 1375		
Gly Pro Phe Thr Gly Pro Glu Cys Gln Phe Pro Ala Ser Ser Pro Cys 1380 1385 1390		
Leu Gly Gly Asn Pro Cys Tyr Asn Gln Gly Thr Cys Glu Pro Thr Ser 1395 1400 1405		
Glu Ser Pro Phe Tyr Arg Cys Leu Cys Pro Ala Lys Phe Asn Gly Leu 1410 1415 1420		
Leu Cys His Ile Leu Asp Tyr Ser Phe Gly Gly Gly Ala Gly Arg Asp 1425 1430 1435 1440		
Ile Pro Pro Pro Leu Ile Glu Glu Ala Cys Glu Leu Pro Glu Cys Gln 1445 1450 1455		
Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn His Ala 1460 1465 1470		
Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp Pro Trp 1475 1480 1485		
Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser Asp Gly 1490 1495 1500		
His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp Gly Phe 1505 1510 1515 1520		
Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp Gln Tyr 1525 1530 1535		
Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys Asn Ser 1540 1545 1550		
Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val Pro Glu 1555 1560 1565		
Arg Leu Ala Ala Gly Thr Leu Val Val Val Val Leu Met Pro Pro Glu 1570 1575 1580		
Gln Leu Arg Asn Ser Ser Phe His Phe Leu Arg Glu Leu Ser Arg Val 1585 1590 1595 1600		
Leu His Thr Asn Val Val Phe Lys Arg Asp Ala His Gly Gln Gln Met 1605 1610 1615		
Ile Phe Pro Tyr Tyr Gly Arg Glu Glu Glu Leu Arg Lys His Pro Ile 1620 1625 1630		
Lys Arg Ala Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu Gly Gln 1635 1640 1645		
Val Lys Ala Ser Leu Leu Pro Gly Gly Ser Glu Gly Gly Arg Arg Arg 1650 1655 1660		
Arg Glu Leu Asp Pro Met Asp Val Arg Gly Ser Ile Val Tyr Leu Glu 1665 1670 1675 1680		
Ile Asp Asn Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe Gln Ser 1685 1690 1695		

Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu Gly Ser
1700 1705 1710

Leu Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu Thr Val Glu
1715 1720 1725

Pro Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val Ala Ala Ala Ala
1730 1735 1740

Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser Arg Lys
1745 1750 1755 1760

Arg Arg Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe Lys Val
1765 1770 1775

Ser Glu Ala Ser Lys Lys Lys Arg Arg Glu Glu Leu Gly Glu Asp Ser
1780 1785 1790

Val Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu Met Asp
1795 1800 1805

Asp Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys Lys Phe
1810 1815 1820

Arg Phe Glu Glu Pro Val Val Leu Pro Asp Leu Asp Asp Gln Thr Asp
1825 1830 1835 1840

His Arg Gln Trp Thr Gln Gln His Leu Asp Ala Ala Asp Leu Arg Met
1845 1850 1855

Ser Ala Met Ala Pro Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys
1860 1865 1870

Met Asp Val Asn Val Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile
1875 1880 1885

Ala Ser Cys Ser Gly Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu
1890 1895 1900

Glu Asp Ala Pro Ala Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser
1905 1910 1915 1920

Leu His Asn Gln Thr Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala
1925 1930 1935

Ala Arg Tyr Ser Arg Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser
1940 1945 1950

Ala Asp Ala Asn Ile Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala
1955 1960 1965

Ala Val Ser Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn
1970 1975 1980

Arg Ala Thr Asp Leu Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu
1985 1990 1995 2000

Ile Leu Ala Ala Arg Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile
2005 2010 2015

Asn Ser His Ala Asp Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala
2020 2025 2030

Leu His Trp Ala Ala Ala Val Asn Asn Val Asp Ala Ala Val Val Leu
2035 2040 2045

Leu Lys Asn Gly Ala Asn Lys Asp Met Gln Asn Asn Arg Glu Glu Thr

2050	2055	2060
Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val 2065	2070	2075 2080
Leu Leu Asp His Phe Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg 2085	2090	2095
Leu Pro Arg Asp Ile Ala Gln Glu Arg Met His His Asp Ile Val Arg 2100	2105	2110
Leu Leu Asp Glu Tyr Asn Leu Val Arg Ser Pro Gln Leu His Gly Ala 2115	2120	2125
Pro Leu Gly Gly Thr Pro Thr Leu Ser Pro Pro Leu Cys Ser Pro Asn 2130	2135	2140
Gly Tyr Leu Gly Ser Leu Lys Pro Gly Val Gln Gly Lys Lys Val Arg 2145	2150	2155 2160
Lys Pro Ser Ser Lys Gly Leu Ala Cys Gly Ser Lys Glu Ala Lys Asp 2165	2170	2175
Leu Lys Ala Arg Arg Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu 2180	2185	2190
Asp Ser Ser Gly Met Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His 2195	2200	2205
Gly Tyr Leu Ser Asp Val Ala Ser Pro Pro Leu Leu Pro Ser Pro Phe 2210	2215	2220
Gln Gln Ser Pro Ser Val Pro Leu Asn His Leu Pro Gly Met Pro Asp 2225	2230	2235 2240
Thr His Leu Gly Ile Gly His Leu Asn Val Ala Ala Lys Pro Glu Met 2245	2250	2255
Ala Ala Leu Gly Gly Gly Gly Arg Leu Ala Phe Glu Thr Gly Pro Pro 2260	2265	2270
Arg Leu Ser His Leu Pro Val Ala Ser Gly Thr Ser Thr Val Leu Gly 2275	2280	2285
Ser Ser Ser Gly Gly Ala Leu Asn Phe Thr Val Gly Gly Ser Thr Ser 2290	2295	2300
Leu Asn Gly Gln Cys Glu Trp Leu Ser Arg Leu Gln Ser Gly Met Val 2305	2310	2315 2320
Pro Asn Gln Tyr Asn Pro Leu Arg Gly Ser Val Ala Pro Gly Pro Leu 2325	2330	2335
Ser Thr Gln Ala Pro Ser Leu Gln His Gly Met Val Gly Pro Leu His 2340	2345	2350
Ser Ser Leu Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr Gln Gly 2355	2360	2365
Leu Pro Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln Thr Gln 2370	2375	2380
Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu Gln Pro 2385	2390	2395 2400
Ala Asn Ile Gln Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro Pro Pro 2405	2410	2415

135

Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu Gly Arg
2420 2425 2430

Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln Pro Leu Gly
2435 2440 2445

Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser Pro Ala
2450 2455 2460

Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr Ala Ala
2465 2470 2475 2480

Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro Val Glu
2485 2490 2495

Asn Thr Pro Ser His Gln Leu Gln Val Pro Glu His Pro Phe Leu Thr
2500 2505 2510

Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser
2515 2520 2525

Asn Val Ser Asp Trp Ser Glu Gly Val Ser Ser Pro Pro Thr Ser Met
2530 2535 2540

Gln Ser Gln Ile Ala Arg Ile Pro Glu Ala Phe Lys
2545 2550 2555

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 10..7419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCG CCC GCC CTG CGC CCC GCT CTG CTG TGG GCG CTG CTG GCG	48
Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala	
1 5 10	
CTC TGG CTG TGC TGC GCG GCC CCC GCG CAT GCA TTG CAG TGT CGA GAT	96
Leu Trp Leu Cys Cys Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp	
15 20 25	
GGC TAT GAA CCC TGT GTA AAT GAA GGA ATG TGT GTT ACC TAC CAC AAT	144
Gly Tyr Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr His Asn	
30 35 40 45	
GGC ACA GGA TAC TGC AAA TGT CCA GAA GGC TTC TTG GGG GAA TAT TGT	192
Gly Thr Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys	
50 55 60	
CAA CAT CGA GAC CCC TGT GAG AAG AAC CGC TGC CAG AAT GGT GGG ACT	240
Gln His Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr	
65 70 75	
TGT GTG GCC CAG GCC ATG CTG GGG AAA GCC ACG TGC CGA TGT GCC TCA	288
Cys Val Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser	

80						85						90						
GGG Gly	TTT Phe	ACA Thr	GGA Gly	GAG Glu	GAC Asp	TGC Cys	CAG Gln	TAC Tyr	TCA Ser	ACA Thr	TCT Ser	CAT His	CCA Pro	TGC Cys	TTT Phe	336		
95						100						105						
GTG Val	TCT Ser	CGA Arg	CCC Pro	TGC Cys	CTG Leu	AAT Asn	GGC Gly	GGC Gly	ACA Thr	TGC Cys	CAT His	ATG Met	CTC Leu	AGC Ser	CGG Arg	384		
110						115						120						
GAT Asp	ACC Thr	TAT Tyr	GAG Glu	TGC Cys	ACC Thr	TGT Cys	CAA Gln	GTC Val	GGG Gly	TTT Phe	ACA Thr	GGT Gly	AAG Lys	GAG Glu	TGC Cys	432		
130						135						140						
CAA Gln	TGG Trp	ACG Thr	GAT Asp	GCC Ala	TGC Cys	CTG Leu	TCT Ser	CAT His	CCC Pro	TGT Cys	GCA Ala	AAT Asn	GGA Gly	AGT Ser	ACC Thr	480		
145						150						155						
TGT Cys	ACC Thr	ACT Thr	GTG Val	GCC Ala	AAC Asn	CAG Gln	TTC Phe	TCC Ser	TGC Cys	AAA Lys	TGC Cys	CTC Leu	ACA Thr	GGC Gly	TTC Phe	528		
160						165						170						
ACA Thr	GGG Gly	CAG Gln	AAA Lys	TGT Cys	GAG Glu	ACT Thr	GAT Asp	GTC Val	AAT Asn	GAG Glu	TGT Cys	GAC Asp	ATT Ile	CCA Pro	GGA Gly	576		
175						180						185						
CAC His	TGC Cys	CAG Gln	CAT His	GGT Gly	GGC Gly	ACC Thr	TGC Cys	CTC Leu	AAC Asn	CTG Leu	CCT Pro	GGT Gly	TCC Ser	TAC Tyr	CAG Gln	624		
190						195						200						
TGC Cys	CAG Gln	TGC Cys	CCT Pro	CAG Gln	GGC Gly	TTC Phe	ACA Thr	GGC Gly	CAG Gln	TAC Tyr	TGT Cys	GAC Asp	AGC Ser	CTG Leu	TAT Tyr	672		
210						215						220						
GTG Val	CCC Pro	TGT Cys	GCA Ala	CCC Pro	TCA Ser	CCT Pro	TGT Cys	GTC Val	AAT Asn	GGA Gly	GGC Gly	ACC Thr	TGT Cys	CGG Arg	CAG Gln	720		
225						230						235						
ACT Thr	GGT Gly	GAC Asp	TTC Phe	ACT Thr	TTT Phe	GAG Glu	TGC Cys	AAC Asn	TGC Cys	CTT Leu	CCA Pro	GGT Gly	TTT Phe	GAA Glu	GGG Gly	768		
240						245						250						
AGC Ser	ACC Thr	TGT Cys	GAG Glu	AGG Arg	AAT Asn	ATT Ile	GAT Asp	GAC Asp	TGC Cys	CCT Pro	AAC Asn	CAC His	AGG Arg	TGT Cys	CAG Gln	816		
255						260						265						
AAT Asn	GGA Gly	GGG Gly	GTT Val	TGT Cys	GTG Val	GAT Asp	GGG Gly	GTC Val	AAC Asn	ACT Thr	TAC Tyr	AAC Asn	TGC Cys	CGC Arg	TGT Cys	864		
270						275						280						
CCC Pro	CCA Pro	CAA Gln	TGG Trp	ACA Thr	GGA Gly	CAG Gln	TTC Phe	TGC Cys	ACA Thr	GAG Glu	GAT Asp	GTG Val	GAT Asp	GAA Glu	TGC Cys	912		
290						295						300						
CTG Leu	CTG Leu	CAG Gln	CCC Pro	AAT Asn	GCC Ala	TGT Cys	CAA Gln	AAT Asn	GGG Gly	GGC Gly	ACC Thr	TGT Cys	GCC Ala	AAC Asn	CGC Arg	960		
305						310						315						
AAT Asn	GGA Gly	GGC Gly	TAT Tyr	GGC Gly	TGT Cys	GTA Val	TGT Cys	GTC Val	AAC Asn	GGC Gly	TGG Trp	AGT Ser	GGA Gly	GAT Asp	GAC Asp	1008		
320						325						330						
TGC Cys	AGT Ser	GAG Glu	AAC Asn	ATT Ile	GAT Asp	GAT Asp	TGT Cys	GCC Ala	TTC Phe	GCC Ala	TCC Ser	TGT Cys	ACT Thr	CCA Pro	GGC Gly	1056		
335						340						345						
TCC ACC	TGC ATC	GAC CGT	GTG GCC	TCC TTC	TCT TGC	ATG TGC	CCA GAG									1104		

Ser 350	Thr	Cys	Ile	Asp	Arg 355	Val	Ala	Ser	Phe	Ser 360	Cys	Met	Cys	Pro	Glu 365	
GGG Gly	AAG Lys	GCA Ala	GGT Gly	CTC Leu 370	CTG Leu	TGT Cys	CAT His	CTG Leu	GAT Asp 375	GAT Asp	GCA Ala	TGC Cys	ATC Ile	AGC Ser 380	AAT Asn	1152
CCT Pro	TGC Cys	CAC His	AAG Lys 385	GGG Gly	GCA Ala	CTG Leu	TGT Cys	GAC Asp 390	ACC Thr	AAC Asn	CCC Pro	CTA Leu	AAT Asn 395	GGG Gly	CAA Gln	1200
TAT Tyr	ATT Ile	TGC Cys 400	ACC Thr	TGC Cys	CCA Pro	CAA Gln	GGC Gly 405	TAC Tyr	AAA Lys	GGG Gly	GCT Ala	GAC Asp 410	TGC Cys	ACA Thr	GAA Glu	1248
GAT Asp	GTG Val 415	GAT Asp	GAA Glu	TGT Cys	GCC Ala	ATG Met 420	GCC Ala	AAT Asn	AGC Ser	AAT Asn	CCT Pro 425	TGT Cys	GAG Glu	CAT His	GCA Ala	1296
GGA Gly 430	AAA Lys	TGT Cys	GTG Val	AAC Asn	ACG Thr 435	GAT Asp	GGC Gly	GCC Ala	TTC Phe	CAC His 440	TGT Cys	GAG Glu	TGT Cys	CTG Leu	AAG Lys 445	1344
GGT Gly	TAT Tyr	GCA Ala	GGA Gly	CCT Pro 450	CGT Arg	TGT Cys	GAG Glu	ATG Met	GAC Asp 455	ATC Ile	AAT Asn	GAG Glu	TGC Cys	CAT His 460	TCA Ser	1392
GAC Asp	CCC Pro	TGC Cys	CAG Gln 465	AAT Asn	GAT Asp	GCT Ala	ACC Thr	TGT Cys 470	CTG Leu	GAT Asp	AAG Lys	ATT Ile	GGA Gly 475	GGC Gly	TTC Phe	1440
ACA Thr	TGT Cys 480	CTG Leu	TGC Cys	ATG Met	CCA Pro	GGT Gly	TTC Phe 485	AAA Lys	GGT Gly	GTG Val	CAT His 490	TGT Cys	GAA Glu	TTA Leu	GAA Glu	1488
ATA Ile 495	AAT Asn	GAA Glu	TGT Cys	CAG Gln	AGC Ser	AAC Asn 500	CCT Pro	TGT Cys	GTG Val	AAC Asn	AAT Asn 505	GGG Gly	CAG Gln	TGT Cys	GTG Val	1536
GAT Asp 510	AAA Lys	GTC Val	AAT Asn	CGT Arg	TTC Phe 515	CAG Gln	TGC Cys	CTG Leu	TGT Cys	CCT Pro 520	CCT Pro	GGT Gly	TTC Phe	ACT Thr	GGG Gly 525	1584
CCA Pro	GTT Val	TGC Cys	CAG Gln 530	ATT Ile	GAT Asp	ATT Ile	GAT Asp	GAC Asp	TGT Cys 535	TCC Ser	AGT Ser	ACT Thr	CCG Pro	TGT Cys 540	CTG Leu	1632
AAT Asn	GGG Gly	GCA Ala	AAG Lys 545	TGT Cys	ATC Ile	GAT Asp	CAC His	CCG Pro 550	AAT Asn	GGC Gly	TAT Tyr	GAA Glu	TGC Cys 555	CAG Gln	TGT Cys	1680
GCC Ala	ACA Thr 560	GGT Gly	TTC Phe	ACT Thr	GGT Gly	GTG Val 565	TTG Leu	TGT Cys	GAG Glu	GAG Glu	AAC Asn 570	ATT Ile	GAC Asp	AAC Asn	TGT Cys	1728
GAC Asp	CCC Pro 575	GAT Asp	CCT Pro	TGC Cys	CAC His	CAT His 580	GGT Gly	CAG Gln	TGT Cys	CAG Gln	GAT Asp 585	GGT Gly	ATT Ile	GAT Asp	TCC Ser	1776
TAC Tyr 590	ACC Thr	TGC Cys	ATC Ile	TGC Cys	AAT Asn 595	CCC Pro	GGG Gly	TAC Tyr	ATG Met	GGC Gly 600	GCC Ala	ATC Ile	TGC Cys	AGT Ser	GAC Asp 605	1824
CAG Gln	ATT Ile	GAT Asp	GAA Glu 610	TGT Cys	TAC Tyr	AGC Ser	AGC Ser	CCT Pro	TGC Cys 615	CTG Leu	AAC Asn	GAT Asp	GGT Gly	CGC Arg 620	TGC Cys	1872

ATT Ile	GAC Asp	CTG Leu	GTC Val 625	AAT Asn	GGC Gly	TAC Tyr	CAG Gln	TGC Cys 630	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GGC Gly 635	ACG Thr	TCA Ser	1920
GGG Gly	GTT Val	AAT Asn 640	TGT Cys	GAA Glu	ATT Ile	AAT Asn	TTT Phe 645	GAT Asp	GAC Asp	TGT Cys	GCA Ala	AGT Ser 650	AAC Asn	CCT Pro	TGT Cys	1968
ATC Ile 655	CAT His	GGA Gly	ATC Ile	TGT Cys	ATG Met	GAT Asp 660	GGC Gly	ATT Ile	AAT Asn	CGC Arg	TAC Tyr 665	AGT Ser	TGT Cys	GTC Val	TGC Cys	2016
TCA Ser 670	CCA Pro	GGA Gly	TTC Phe	ACA Thr	GGG Gly 675	CAG Gln	AGA Arg	TGT Cys	AAC Asn	ATT Ile 680	GAC Asp	ATT Ile	GAT Asp	GAG Glu	TGT Cys 685	2064
GCC Ala	TCC Ser	AAT Asn	CCC Pro	TGT Cys 690	CGC Arg	AAG Lys	GGT Gly	GCA Ala	ACA Thr 695	TGT Cys	ATC Ile	AAC Asn	GGT Gly	GTG Val 700	AAT Asn	2112
GGT Gly	TTC Phe	CGC Arg	TGT Cys 705	ATA Ile	TGC Cys	CCC Pro	GAG Glu	GGA Gly 710	CCC Pro	CAT His	CAC His	CCC Pro	AGC Ser 715	TGC Cys	TAC Tyr	2160
TCA Ser	CAG Gln 720	GTG Val	AAC Asn	GAA Glu	TGC Cys	CTG Leu	AGC Ser 725	AAT Asn	CCC Pro	TGC Cys	ATC Ile	CAT His 730	GGA Gly	AAC Asn	TGT Cys	2208
ACT Thr 735	GGA Gly	GGT Gly	CTC Leu	AGT Ser	GGA Gly	TAT Tyr 740	AAG Lys	TGT Cys	CTC Leu	TGT Cys	GAT Asp 745	GCA Ala	GGC Gly	TGG Trp	GTT Val	2256
GGC Gly 750	ATC Ile	AAC Asn	TGT Cys	GAA Glu	GTG Val 755	GAC Asp	AAA Lys	AAT Asn	GAA Glu	TGC Cys 760	CTT Leu	TCG Ser	AAT Asn	CCA Pro	TGC Cys 765	2304
CAG Gln	AAT Asn	GGA Gly	GGA Gly	ACT Thr 770	TGT Cys	GAC Asp	AAT Asn	CTG Leu	GTG Val 775	AAT Asn	GGA Gly	TAC Tyr	AGG Arg	TGT Cys 780	ACT Thr	2352
TGC Cys	AAG Lys	AAG Lys	GGC Gly 785	TTT Phe	AAA Lys	GGC Gly	TAT Tyr	AAC Asn 790	TGC Cys	CAG Gln	GTG Val	AAT Asn	ATT Ile 795	GAT Asp	GAA Glu	2400
TGT Cys	GCC Ala	TCA Ser 800	AAT Asn	CCA Pro	TGC Cys	CTG Leu	AAC Asn 805	CAA Gln	GGA Gly	ACC Thr	TGC Cys	TTT Phe 810	GAT Asp	GAC Asp	ATA Ile	2448
AGT Ser 815	GGC Gly	TAC Tyr	ACT Thr	TGC Cys	CAC His	TGT Cys 820	GTG Val	CTG Leu	CCA Pro	TAC Tyr	ACA Thr 825	GGC Gly	AAG Lys	AAT Asn	TGT Cys	2496
CAG Gln 830	ACA Thr	GTA Val	TTG Leu	GCT Ala	CCC Pro 835	TGT Cys	TCC Ser	CCA Pro	AAC Asn	CCT Pro 840	TGT Cys	GAG Glu	AAT Asn	GCT Ala 845	GCT Ala	2544
GTT Val	TGC Cys	AAA Lys	GAG Glu	TCA Ser 850	CCA Pro	AAT Asn	TTT Phe	GAG Glu	AGT Ser 855	TAT Tyr	ACT Thr	TGC Cys	TTG Leu	TGT Cys 860	GCT Ala	2592
CCT Pro	GGC Gly	TGG Trp	CAA Gln 865	GGT Gly	CAG Gln	CGG Arg	TGT Cys 870	ACC Thr	ATT Ile	GAC Asp	ATT Ile	GAC Asp	GAG Glu 875	TGT Cys	ATC Ile	2640
TCC Ser	AAG Lys	CCC Pro 880	TGC Cys	ATG Met	AAC Asn	CAT His	GGT Gly 885	CTC Leu	TGC Cys	CAT His	AAC Asn	ACC Thr 890	CAG Gln	GGC Gly	AGC Ser	2688

TAC Tyr 895	ATG Met	TGT Cys	GAA Glu	TGT Cys	CCA Pro	CCA Pro 900	GGC Gly	TTC Phe	AGT Ser	GGT Gly	ATG Met 905	GAC Asp	TGT Cys	GAG Glu	GAG Glu	2736
GAC Asp 910	ATT Ile	GAT Asp	GAC Asp	TGC Cys	CTT Leu 915	GCC Ala	AAT Asn	CCT Pro	TGC Cys	CAG Gln 920	AAT Asn	GGA Gly	GGT Gly	TCC Ser	TGT Cys 925	2784
ATG Met	GAT Asp	GGA Gly	GTG Val	AAT Asn 930	ACT Thr	TTC Phe	TCC Ser	TGC Cys	CTC Leu 935	TGC Cys	CTT Leu	CCG Pro	GGT Gly	TTC Phe 940	ACT Thr	2832
GGG Gly	GAT Asp	AAG Lys	TGC Cys 945	CAG Gln	ACA Thr	GAC Asp	ATG Met 950	AAT Asn	GAG Glu	TGT Cys	CTG Leu	AGT Ser	GAA Glu 955	CCC Pro	TGT Cys	2880
AAG Lys	AAT Asn	GGA Gly 960	GGG Gly	ACC Thr	TGC Cys	TCT Ser	GAC Asp 965	TAC Tyr	GTC Val	AAC Asn	AGT Ser	TAC Tyr 970	ACT Thr	TGC Cys	AAG Lys	2928
TGC Cys 975	CAG Gln	GCA Ala	GGA Gly	TTT Phe	GAT Asp	GGA Gly 980	GTC Val	CAT His	TGT Cys	GAG Glu	AAC Asn 985	AAC Asn	ATC Ile	AAT Asn	GAG Glu	2976
TGC Cys 990	ACT Thr	GAG Glu	AGC Ser	TCC Ser	TGT Cys 995	TTC Phe	AAT Asn	GGT Gly	GGC Gly	ACA Thr 1000	TGT Cys	GTT Val	GAT Asp	GGG Gly	ATT Ile 1005	3024
AAC Asn	TCC Ser	TTC Phe	TCT Ser	TGC Cys 1010	TTG Leu	TGC Cys	CCT Pro	GTG Val	GGT Gly 1015	TTC Phe	ACT Thr	GGA Gly	TCC Ser	TTC Phe 1020	TGC Cys	3072
CTC Leu	CAT His	GAG Glu	ATC Ile 1025	AAT Asn	GAA Glu	TGC Cys	AGC Ser	TCT Ser 1030	CAT His	CCA Pro	TGC Cys	CTG Leu	AAT Asn 1035	GAG Glu	GGA Gly	3120
ACG Thr	TGT Cys	GTT Val 1040	GAT Asp	GGC Gly	CTG Leu	GGT Gly	ACC Thr 1045	TAC Tyr	CGC Arg	TGC Cys	AGC Ser	TGC Cys 1050	CCC Pro	CTG Leu	GGC Gly	3168
TAC Tyr 1055	ACT Thr	GGG Gly	AAA Lys	AAC Asn	TGT Cys	CAG Gln 1060	ACC Thr	CTG Leu	GTG Val	AAT Asn	CTC Leu 1065	TGC Cys	AGT Ser	CGG Arg	TCT Ser	3216
CCA Pro 1070	TGT Cys	AAA Lys	AAC Asn	AAA Lys	GGT Gly 1075	ACT Thr	TGT Cys	GTT Val	CAG Gln 1080	AAA Lys	AAA Lys	GCA Ala	GAG Glu	TCC Ser	CAG Gln 1085	3264
TGC Cys	CTA Leu	TGT Cys	CCA Pro	TCT Ser 1090	GGA Gly	TGG Trp	GCT Ala	GGT Gly	GCC Ala 1095	TAT Tyr	TGT Cys	GAC Asp	GTG Val	CCC Pro 1100	AAT Asn	3312
GTC Val	TCT Ser	TGT Cys	GAC Asp 1105	ATA Ile	GCA Ala	GCC Ala	TCC Ser	AGG Arg 1110	AGA Arg	GGT Gly	GTG Val	CTT Leu	GTT Val 1115	GAA Glu	CAC His	3360
TTG Leu	TGC Cys	CAG Gln 1120	CAC His	TCA Ser	GGT Gly	GTC Val	TGC Cys 1125	ATC Ile	AAT Asn	GCT Ala	GGC Gly 1130	AAC Asn	ACG Thr	CAT His	TAC Tyr	3408
TGT Cys 1135	CAG Gln	TGC Cys	CCC Pro	CTG Leu	GGC Gly	TAT Tyr 1140	ACT Thr	GGG Gly	AGC Ser	TAC Tyr	TGT Cys 1145	GAG Glu	GAG Glu	CAA Gln	CTC Leu	3456
GAT Asp 1150	GAG Glu	TGT Cys	GCG Ala	TCC Ser	AAC Asn 1155	CCC Pro	TGC Cys	CAG Gln	CAC His	GGG Gly 1160	GCA Ala	ACA Thr	TGC Cys	AGT Ser	GAC Asp 1165	3504

TTC ATT GGT GGA TAC AGA TGC GAG TGT GTC CCA GGC TAT CAG GGT GTC Phe Ile Gly Gly Tyr Arg Cys Glu Cys Val Pro Gly Tyr Gln Gly Val 1170 1175 1180	3552
AAC TGT GAG TAT GAA GTG GAT GAG TGC CAG AAT CAG CCC TGC CAG AAT Asn Cys Glu Tyr Glu Val Asp Glu Cys Gln Asn Gln Pro Cys Gln Asn 1185 1190 1195	3600
GGA GGC ACC TGT ATT GAC CTT GTG AAC CAT TTC AAG TGC TCT TGC CCA Gly Gly Thr Cys Ile Asp Leu Val Asn His Phe Lys Cys Ser Cys Pro 1200 1205 1210	3648
CCA GGC ACT CGG GGC CTA CTC TGT GAA GAG AAC ATT GAT GAC TGT GCC Pro Gly Thr Arg Gly Leu Leu Cys Glu Glu Asn Ile Asp Asp Cys Ala 1215 1220 1225	3696
CGG GGT CCC CAT TGC CTT AAT GGT GGT CAG TGC ATG GAT AGG ATT GGA Arg Gly Pro His Cys Leu Asn Gly Gly Gln Cys Met Asp Arg Ile Gly 1230 1235 1240 1245	3744
GGC TAC AGT TGT CGC TGC TTG CCT GGC TTT GCT GGG GAG CGT TGT GAG Gly Tyr Ser Cys Arg Cys Leu Pro Gly Phe Ala Gly Glu Arg Cys Glu 1250 1255 1260	3792
GGA GAC ATC AAC GAG TGC CTC TCC AAC CCC TGC AGC TCT GAG GGC AGC Gly Asp Ile Asn Glu Cys Leu Ser Asn Pro Cys Ser Ser Glu Gly Ser 1265 1270 1275	3840
CTG GAC TGT ATA CAG CTC ACC AAT GAC TAC CTG TGT GTT TGC CGT AGT Leu Asp Cys Ile Gln Leu Thr Asn Asp Tyr Leu Cys Val Cys Arg Ser 1280 1285 1290	3888
GCC TTT ACT GGC CGG CAC TGT GAA ACC TTC GTC GAT GTG TGT CCC CAG Ala Phe Thr Gly Arg His Cys Glu Thr Phe Val Asp Val Cys Pro Gln 1295 1300 1305	3936
ATG CCC TGC CTG AAT GGA GGG ACT TGT GCT GTG GCC AGT AAC ATG CCT Met Pro Cys Leu Asn Gly Gly Thr Cys Ala Val Ala Ser Asn Met Pro 1310 1315 1320 1325	3984
GAT GGT TTC ATT TGC CGT TGT CCC CCG GGA TTT TCC GGG GCA AGG TGC Asp Gly Phe Ile Cys Arg Cys Pro Pro Gly Phe Ser Gly Ala Arg Cys 1330 1335 1340	4032
CAG AGC AGC TGT GGA CAA GTG AAA TGT AGG AAG GGG GAG CAG TGT GTG Gln Ser Ser Cys Gly Gln Val Lys Cys Arg Lys Gly Glu Gln Cys Val 1345 1350 1355	4080
CAC ACC GCC TCT GGA CCC CGC TGC TTC TGC CCC AGT CCC CGG GAC TGC His Thr Ala Ser Gly Pro Arg Cys Phe Cys Pro Ser Pro Arg Asp Cys 1360 1365 1370	4128
GAG TCA GGC TGT GCC AGT AGC CCC TGC CAG CAC GGG GGC AGC TGC CAC Glu Ser Gly Cys Ala Ser Ser Pro Cys Gln His Gly Gly Ser Cys His 1375 1380 1385	4176
CCT CAG CGC CAG CCT CCT TAT TAC TCC TGC CAG TGT GCC CCA CCA TTC Pro Gln Arg Gln Pro Pro Tyr Tyr Ser Cys Gln Cys Ala Pro Pro Phe 1390 1395 1400 1405	4224
TCG GGT AGC CGC TGT GAA CTC TAC ACG GCA CCC CCC AGC ACC CCT CCT Ser Gly Ser Arg Cys Glu Leu Tyr Thr Ala Pro Pro Ser Thr Pro Pro 1410 1415 1420	4272
GCC ACC TGT CTG AGC CAG TAT TGT GCC GAC AAA GCT CGG GAT GGC GTC Ala Thr Cys Leu Ser Gln Tyr Cys Ala Asp Lys Ala Arg Asp Gly Val 1425 1430 1435	4320

TGT Cys	GAT Asp	GAG Glu	GCC Ala	TGC Cys	AAC Asn	AGC Ser	CAT His	GCC Ala	TGC Cys	CAG Gln	TGG Trp	GAT Asp	GGG Gly	GGT Gly	GAC Asp	4368
		1440					1445					1450				
TGT Cys	TCT Ser	CTC Leu	ACC Thr	ATG Met	GAG Glu	AAC Asn	CCC Pro	TGG Trp	GCC Ala	AAC Asn	TGC Cys	TCC Ser	TCC Ser	CCA Pro	CTT Leu	4416
	1455					1460					1465					
CCC Pro	TGC Cys	TGG Trp	GAT Asp	TAT Tyr	ATC Ile	AAC Asn	AAC Asn	CAG Gln	TGT Cys	GAT Asp	GAG Glu	CTG Leu	TGC Cys	AAC Asn	ACG Thr	4464
1470					1475					1480					1485	
GTC Val	GAG Glu	TGC Cys	CTG Leu	TTT Phe	GAC Asp	AAC Asn	TTT Phe	GAA Glu	TGC Cys	CAG Gln	GGG Gly	AAC Asn	AGC Ser	AAG Lys	ACA Thr	4512
				1490				1495						1500		
TGC Cys	AAG Lys	TAT Tyr	GAC Asp	AAA Lys	TAC Tyr	TGT Cys	GCA Ala	GAC Asp	CAC His	TTC Phe	AAA Lys	GAC Asp	AAC Asn	CAC His	TGT Cys	4560
			1505					1510					1515			
AAC Asn	CAG Gln	GGG Gly	TGC Cys	AAC Asn	AGT Ser	GAG Glu	GAG Glu	TGT Cys	GGT Gly	TGG Trp	GAT Asp	GGG Gly	CTG Leu	GAC Asp	TGT Cys	4608
		1520					1525					1530				
GCT Ala	GCT Ala	GAC Asp	CAA Gln	CCT Pro	GAG Glu	AAC Asn	CTG Leu	GCA Ala	GAA Glu	GGT Gly	ACC Thr	CTG Leu	GTT Val	ATT Ile	GTG Val	4656
	1535					1540					1545					
GTA Val	TTG Leu	ATG Met	CCA Pro	CCT Pro	GAA Glu	CAA Gln	CTG Leu	CTC Leu	CAG Gln	GAT Asp	GCT Ala	CGC Arg	AGC Ser	TTC Phe	TTG Leu	4704
1550					1555					1560					1565	
CGG Arg	GCA Ala	CTG Leu	GGT Gly	ACC Thr	CTG Leu	CTC Leu	CAC His	ACC Thr	AAC Asn	CTG Leu	CGC Arg	ATT Ile	AAG Lys	CGG Arg	GAC Asp	4752
				1570					1575					1580		
TCC Ser	CAG Gln	GGG Gly	GAA Glu	CTC Leu	ATG Met	GTG Val	TAC Tyr	CCC Pro	TAT Tyr	TAT Tyr	GGT Gly	GAG Glu	AAG Lys	TCA Ser	GCT Ala	4800
		1585					1590						1595			
GCT Ala	ATG Met	AAG Lys	AAA Lys	CAG Gln	AGG Arg	ATG Met	ACA Thr	CGC Arg	AGA Arg	TCC Ser	CTT Leu	CCT Pro	GGT Gly	GAA Glu	CAA Gln	4848
		1600					1605					1610				
GAA Glu	CAG Gln	GAG Glu	GTG Val	GCT Ala	GGC Gly	TCT Ser	AAA Lys	GTC Val	TTT Phe	CTG Leu	GAA Glu	ATT Ile	GAC Asp	AAC Asn	CGC Arg	4896
	1615					1620					1625					
CAG Gln	TGT Cys	GTT Val	CAA Gln	GAC Asp	TCA Ser	GAC Asp	CAC His	TGC Cys	TTC Phe	AAG Lys	AAC Asn	ACG Thr	GAT Asp	GCA Ala	GCA Ala	4944
1630					1635					1640					1645	
GCA Ala	GCT Ala	CTC Leu	CTG Leu	GCC Ala	TCT Ser	CAC His	GCC Ala	ATA Ile	CAG Gln	GGG Gly	ACC Thr	CTG Leu	TCA Ser	TAC Tyr	CCT Pro	4992
				1650					1655					1660		
CTT Leu	GTG Val	TCT Ser	GTC Val	GTC Val	AGT Ser	GAA Glu	TCC Ser	CTG Leu	ACT Thr	CCA Pro	GAA Glu	CGC Arg	ACT Thr	CAG Gln	CTC Leu	5040
			1665					1670					1675			
CTC Leu	TAT Tyr	CTC Leu	CTT Leu	GCT Ala	GTT Val	GCT Ala	GTT Val	GTC Val	ATC Ile	ATT Ile	CTG Leu	TTT Phe	ATT Ile	ATT Ile	CTG Leu	5088
		1680					1685					1690				
CTG Leu	GGG Gly	GTA Val	ATC Ile	ATG Met	GCA Ala	AAA Lys	CGA Arg	AAG Lys	CGT Arg	AAG Lys	CAT His	GGC Gly	TCT Ser	CTC Leu	TGG Trp	5136
	1695					1700					1705					

CTG CCT GAA GGT TTC ACT CTT CGC CGA GAT GCA AGC AAT CAC AAG CGT Leu Pro Glu Gly Phe Thr Leu Arg Arg Asp Ala Ser Asn His Lys Arg 1710 1715 1720 1725	5184
CGT GAG CCA GTG GGA CAG GAT GCT GTG GGG CTG AAA AAT CTC TCA GTG Arg Glu Pro Val Gly Gln Asp Ala Val Gly Leu Lys Asn Leu Ser Val 1730 1735 1740	5232
CAA GTC TCA GAA GCT AAC CTA ATT GGT ACT GGA ACA AGT GAA CAC TGG Gln Val Ser Glu Ala Asn Leu Ile Gly Thr Gly Thr Ser Glu His Trp 1745 1750 1755	5280
GTC GAT GAT GAA GGG CCC CAG CCA AAG AAA GTA AAG GCT GAA GAT GAG Val Asp Asp Glu Gly Pro Gln Pro Lys Lys Val Lys Ala Glu Asp Glu 1760 1765 1770	5328
GCC TTA CTC TCA GAA GAA GAT GAC CCC ATT GAT CGA CGG CCA TGG ACA Ala Leu Leu Ser Glu Glu Asp Asp Pro Ile Asp Arg Arg Pro Trp Thr 1775 1780 1785	5376
CAG CAG CAC CTT GAA GCT GCA GAC ATC CGT AGG ACA CCA TCG CTG GCT Gln Gln His Leu Glu Ala Ala Asp Ile Arg Arg Thr Pro Ser Leu Ala 1790 1795 1800 1805	5424
CTC ACC CCT CCT CAG GCA GAG CAG GAG GTG GAT GTG TTA GAT GTG AAT Leu Thr Pro Pro Gln Ala Glu Gln Glu Val Asp Val Leu Asp Val Asn 1810 1815 1820	5472
GTC CGT GGC CCA GAT GGC TGC ACC CCA TTG ATG TTG GCT TCT CTC CGA Val Arg Gly Pro Asp Gly Cys Thr Pro Leu Met Leu Ala Ser Leu Arg 1825 1830 1835	5520
GGA GGC AGC TCA GAT TTG AGT GAT GAA GAT GAA GAT GCA GAG GAC TCT Gly Gly Ser Ser Asp Leu Ser Asp Glu Asp Glu Asp Ala Glu Asp Ser 1840 1845 1850	5568
TCT GCT AAC ATC ATC ACA GAC TTG GTC TAC CAG GGT GCC AGC CTC CAG Ser Ala Asn Ile Ile Thr Asp Leu Val Tyr Gln Gly Ala Ser Leu Gln 1855 1860 1865	5616
GCC CAG ACA GAC CGG ACT GGT GAG ATG GCC CTG CAC CTT GCA GCC CGC Ala Gln Thr Asp Arg Thr Gly Glu Met Ala Leu His Leu Ala Ala Arg 1870 1875 1880 1885	5664
TAC TCA CGG GCT GAT GCT GCC AAG CGT CTC CTG GAT GCA GGT GCA GAT Tyr Ser Arg Ala Asp Ala Ala Lys Arg Leu Leu Asp Ala Gly Ala Asp 1890 1895 1900	5712
GCC AAT GCC CAG GAC AAC ATG GGC CGC TGT CCA CTC CAT GCT GCA GTG Ala Asn Ala Gln Asp Asn Met Gly Arg Cys Pro Leu His Ala Ala Val 1905 1910 1915	5760
GCA GCT GAT GCC CAA GGT GTC TTC CAG ATT CTG ATT CGC AAC CGA GTA Ala Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Val 1920 1925 1930	5808
ACT GAT CTA GAT GCC AGG ATG AAT GAT GGT ACT ACA CCC CTG ATC CTG Thr Asp Leu Asp Ala Arg Met Asn Asp Gly Thr Thr Pro Leu Ile Leu 1935 1940 1945	5856
GCT GCC CGC CTG GCT GTG GAG GGA ATG GTG GCA GAA CTG ATC AAC TGC Ala Ala Arg Leu Ala Val Glu Gly Met Val Ala Glu Leu Ile Asn Cys 1950 1955 1960 1965	5904
CAA GCG GAT GTG AAT GCA GTG GAT GAC CAT GGA AAA TCT GCT CTT CAC Gln Ala Asp Val Asn Ala Val Asp Asp His Gly Lys Ser Ala Leu His 1970 1975 1980	5952

143

TGG	GCA	GCT	GCT	GTC	AAT	AAT	GTG	GAG	GCA	ACT	CTT	TTG	TTG	TTG	AAA	6000
Trp	Ala	Ala	Ala	Val	Asn	Asn	Val	Glu	Ala	Thr	Leu	Leu	Leu	Leu	Lys	
			1985					1990							1995	
AAT	GGG	GCC	AAC	CGA	GAC	ATG	CAG	GAC	AAC	AAG	GAA	GAG	ACA	CCT	CTG	6048
Asn	Gly	Ala	Asn	Arg	Asp	Met	Gln	Asp	Asn	Lys	Glu	Glu	Thr	Pro	Leu	
		2000					2005					2010				
TTT	CTT	GCT	GCC	CGG	GAG	GGG	AGC	TAT	GAA	GCA	GCC	AAG	ATC	CTG	TTA	6096
Phe	Leu	Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Ala	Ala	Lys	Ile	Leu	Leu	
	2015					2020					2025					
GAC	CAT	TTT	GCC	AAT	CGA	GAC	ATC	ACA	GAC	CAT	ATG	GAT	CGT	CTT	CCC	6144
Asp	His	Phe	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg	Leu	Pro	
2030					2035					2040					2045	
CGG	GAT	GTG	GCT	CGG	GAT	CGC	ATG	CAC	CAT	GAC	ATT	GTG	CGC	CTT	CTG	6192
Arg	Asp	Val	Ala	Arg	Asp	Arg	Met	His	His	Asp	Ile	Val	Arg	Leu	Leu	
				2050						2055				2060		
GAT	GAA	TAC	AAT	GTG	ACC	CCA	AGC	CCT	CCA	GGC	ACC	GTG	TTG	ACT	TCT	6240
Asp	Glu	Tyr	Asn	Val	Thr	Pro	Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser	
			2065					2070					2075			
GCT	CTC	TCA	CCT	GTC	ATC	TGT	GGG	CCC	AAC	AGA	TCT	TTC	CTC	AGC	CTG	6288
Ala	Leu	Ser	Pro	Val	Ile	Cys	Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	
		2080					2085					2090				
AAG	CAC	ACC	CCA	ATG	GGC	AAG	AAG	TCT	AGA	CGG	CCC	AGT	GCC	AAG	AGT	6336
Lys	His	Thr	Pro	Met	Gly	Lys	Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	
	2095					2100					2105					
ACC	ATG	CCT	ACT	AGC	CTC	CCT	AAC	CTT	GCC	AAG	GAG	GCA	AAG	GAT	GCC	6384
Thr	Met	Pro	Thr	Ser	Leu	Pro	Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	
2110					2115					2120					2125	
AAG	GGT	AGT	AGG	AGG	AAG	AAG	TCT	CTG	AGT	GAG	AAG	GTC	CAA	CTG	TCT	6432
Lys	Gly	Ser	Arg	Arg	Lys	Lys	Ser	Leu	Ser	Glu	Lys	Val	Gln	Leu	Ser	
				2130				2135					2140			
GAG	AGT	TCA	GTA	ACT	TTA	TCC	CCT	GTT	GAT	TCC	CTA	GAA	TCT	CCT	CAC	6480
Glu	Ser	Ser	Val	Thr	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	
			2145					2150					2155			
ACG	TAT	GTT	TCC	GAC	ACC	ACA	TCC	TCT	CCA	ATG	ATT	ACA	TCC	CCT	GGG	6528
Thr	Tyr	Val	Ser	Asp	Thr	Thr	Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	
		2160					2165					2170				
ATC	TTA	CAG	GCC	TCA	CCC	AAC	CCT	ATG	TTG	GCC	ACT	GCC	GCC	CCT	CCT	6576
Ile	Leu	Gln	Ala	Ser	Pro	Asn	Pro	Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	
	2175					2180					2185					
GCC	CCA	GTC	CAT	GCC	CAG	CAT	GCA	CTA	TCT	TTT	TCT	AAC	CTT	CAT	GAA	6624
Ala	Pro	Val	His	Ala	Gln	His	Ala	Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	
2190					2195					2200					2205	
ATG	CAG	CCT	TTG	GCA	CAT	GGG	GCC	AGC	ACT	GTG	CTT	CCC	TCA	GTG	AGC	6672
Met	Gln	Pro	Leu	Ala	His	Gly	Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	
				2210					2215				2220			
CAG	TTG	CTA	TCC	CAC	CAC	CAC	ATT	GTG	TCT	CCA	GGC	AGT	GGC	AGT	GCT	6720
Gln	Leu	Leu	Ser	His	His	His	Ile	Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	
			2225					2230					2235			
GGA	AGC	TTG	AGT	AGG	CTC	CAT	CCA	GTC	CCA	GTC	CCA	GCA	GAT	TGG	ATG	6768
Gly	Ser	Leu	Ser	Arg	Leu	His	Pro	Val	Pro	Val	Pro	Ala	Asp	Trp	Met	
		2240					2245					2250				

144

AAC CGC ATG GAG GTG AAT GAG ACC CAG TAC AAT GAG ATG TTT GGT ATG Asn Arg Met Glu Val Asn Glu Thr Gln Tyr Asn Glu Met Phe Gly Met 2255 2260 2265	6816
GTC CTG GCT CCA GCT GAG GGC ACC CAT CCT GGC ATA GCT CCC CAG AGC Val Leu Ala Pro Ala Glu Gly Thr His Pro Gly Ile Ala Pro Gln Ser 2270 2275 2280 2285	6864
AGG COA CCT GAA GGG AAG CAC ATA ACC ACC CCT CGG GAG CCC TTG CCC Arg Pro Pro Glu Gly Lys His Ile Thr Thr Pro Arg Glu Pro Leu Pro 2290 2295 2300	6912
CCC ATT GTG ACT TTC CAG CTC ATC CCT AAA GGC AGT ATT GCC CAA CCA Pro Ile Val Thr Phe Gln Leu Ile Pro Lys Gly Ser Ile Ala Gln Pro 2305 2310 2315	6960
GCG GGG GCT CCC CAG CCT CAG TCC ACC TGC CCT CCA GCT GTT GCG GGC Ala Gly Ala Pro Gln Pro Gln Ser Thr Cys Pro Pro Ala Val Ala Gly 2320 2325 2330	7008
CCC CTG CCC ACC ATG TAC CAG ATT CCA GAA ATG GCC CGT TTG CCC AGT Pro Leu Pro Thr Met Tyr Gln Ile Pro Glu Met Ala Arg Leu Pro Ser 2335 2340 2345	7056
GTG GCT TTC CCC ACT GCC ATG ATG CCC CAG CAG GAC GGG CAG GTA GCT Val Ala Phe Pro Thr Ala Met Met Pro Gln Gln Asp Gly Gln Val Ala 2350 2355 2360 2365	7104
CAG ACC ATT CTC CCA GCC TAT CAT CCT TTC CCA GCC TCT GTG GGC AAG Gln Thr Ile Leu Pro Ala Tyr His Pro Phe Pro Ala Ser Val Gly Lys 2370 2375 2380	7152
TAC CCC ACA CCC CCT TCA CAG CAC AGT TAT GCT TCC TCA AAT GCT GCT Tyr Pro Thr Pro Pro Ser Gln His Ser Tyr Ala Ser Ser Asn Ala Ala 2385 2390 2395	7200
GAG CGA ACA CCC AGT CAC AGT GGT CAC CTC CAG GGT GAG CAT CCC TAC Glu Arg Thr Pro Ser His Ser Gly His Leu Gln Gly Glu His Pro Tyr 2400 2405 2410	7248
CTG ACA CCA TCC CCA GAG TCT CCT GAC CAG TGG TCA AGT TCA TCA CCC Leu Thr Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro 2415 2420 2425	7296
CAC TCT GCT TCT GAC TGG TCA GAT GTG ACC ACC AGC CCT ACC CCT GGG His Ser Ala Ser Asp Trp Ser Asp Val Thr Thr Ser Pro Thr Pro Gly 2430 2435 2440 2445	7344
GGT GCT GGA GGA GGT CAG CGG GGA CCT GGG ACA CAC ATG TCT GAG CCA Gly Ala Gly Gly Gly Gln Arg Gly Pro Gly Thr His Met Ser Glu Pro 2450 2455 2460	7392
CCA CAC AAC AAC ATG CAG GTT TAT GCG TGAGAGAGTC CACCTCCAGT Pro His Asn Asn Met Gln Val Tyr Ala 2465 2470	7439
GTAGAGACAT AACTGACTTT TGTAATGCT GCTGAGGAAC AAATGAAGGT CATCCGGGAG	7499
AGAAATGAAG AAATCTCTGG AGCCAGCTTC TAGAGGTAGG AAAGAGAAGA TGTTCTTATT	7559
CAGATAATGC AAGAGAAGCA ATTCGTCAGT TTTACTGGGT ATCTGCAAGG CTTATTGATT	7619
ATTCTAATCT AATAAGACAA GTTTGTGGAA ATGCAAGATG AATACAAGCC TTGGGTCCAT	7679
GTTTACTCTC TTCTATTTGG AGAATAAGAT GGATGCTTAT TGAAGCCCAG ACATTCTTGC	7739
AGCTTGGACT GCATTTTAAG CCCTGCAGGC TTCTGCCATA TCCATGAGAA GATTCTACAC	7799

TAGCGTCCTG	TTGGGAATTA	TGCCCTGGAA	TTCTGCCTGA	ATTGACCTAC	GCATCTCCTC	7859
CTCCTTGGAC	ATTCTTTTGT	CTTCATTTGG	TGCTTTTGGT	TTTGACCTC	TCCGTGATTG	7919
TAGCCCTACC	AGCATGTTAT	AGGGCAAGAC	CTTTGTGCTT	TTGATCATT	TGGCCCATGA	7979
AAGCAACTTT	GGTCTCCTTT	CCCCTCCTGT	CTTCCCGGTA	TCCCTTGGAG	TCTCACAAGG	8039
TTTACTTTGG	TATGGTTCTC	AGCACAAACC	TTTCAAGTAT	GTTGTTTCTT	TGGAAAATGG	8099
ACATACTGTA	TTGTGTTCTC	CTGCATATAT	CATTCCTGGA	GAGAGAAGGG	GAGAAGAATA	8159
CTTTTCTTCA	ACAAATTTTG	GGGGCAGGAG	ATCCCTTCAA	GAGGCTGCAC	CTTAATTTTT	8219
CTTGTCTGTG	TGCAGGTCTT	CATATAAACT	TTACCAGGAA	GAAGGGTGTG	AGTTTGTTGT	8279
TTTTCTGTGT	ATGGGCCTGG	TCAGTGTAAG	GTTTTATCCT	TGATAGTCTA	GTTACTATGA	8339
CCCTCCCCAC	TTTTTTAAAA	CCAGAAAAAG	GTTTGGAATG	TTGGAATGAC	CAAGAGACAA	8399
GTTAACTCGT	GCAAGAGCCA	GTTACCCACC	CACAGGTCCC	CCTACTTCCT	GCCAAGCATT	8459
CCATTGACTG	CCTGTATGGA	ACACATTTGT	CCCAGATCTG	AGCATTCTAG	GCCTGTTTCA	8519
CTCACTCACC	CAGCATATGA	AACTAGTCTT	AACTGTTGAG	CCTTTCCTTT	CATATCCACA	8579
GAAGACACTG	TCTCAAATGT	TGTACCCTTG	CCATTTAGGA	CTGAACCTTC	CTTAGCCCAA	8639
GGGACCCAGT	GACAGTTGTC	TTCCGTTTGT	CAGATGATCA	GTCTCTACTG	ATTATCTTGC	8699
TGCTTAAAGG	CCTGCTCACC	AATCTTTCTT	TCACACCGTG	TGGTCCGTGT	TACTGGTATA	8759
CCCAGTATGT	TCTCACTGAA	GACATGGACT	TTATATGTTC	AAGTGCAGGA	ATTGGAAAGT	8819
TGGACTTGTT	TTCTATGATC	CAAACAGCC	CTATAAGAAG	GTTGGAAAAG	GAGGAACTAT	8879
ATAGCAGCCT	TTGCTATTTT	CTGCTACCAT	TTCTTTTCCT	CTGAAGCGGC	CATGACATTC	8939
CCTTTGGCAA	CTAACGTAGA	AACTCAACAG	AACATTTTCC	TTTCCTAGAG	TCACCTTTTA	8999
GATGATAATG	GACAACTATA	GACTTGCTCA	TTGTTTCAGAC	TGATTGCCCC	TCACCTGAAT	9059
CCACTCTCTG	TATTCATGCT	CTTGGCAATT	TCTTTGACTT	TCTTTTAAGG	GCAGAAGCAT	9119
TTTAGTTAAT	TGTAGATAAA	GAATAGTTTT	CTTCCTCTTC	TCCTTGGGCC	AGTTAATAAT	9179
TGGTCCATGG	CTACACTGCA	ACTTCCGTCC	AGTGCTGTGA	TGCCCATGAC	ACCTGCAAAA	9239
TAAGTTCTGC	CTGGGCATTT	TGTAGATATT	AACAGGTGAA	TTCCCGACTC	TTTTGGTTTG	9299
AATGACAGTT	CTCATTCCTT	CTATGGCTGC	AAGTATGCAT	CAGTGCTTCC	CACTTACCTG	9359
ATTGTCTGT	CGGTGGCCCC	ATATGGAAAC	CCTGCGTGTC	TGTTGGCATA	ATAGTTTACA	9419
AATGGTTTTT	TCAGTCCTAT	CCAAATTTAT	TGAACCAACA	AAAATAATTA	CTTCTGCCCT	9479
GAGATAAGCA	GATTAAGTTT	GTTCAATCTC	TGCTTTATTC	TCTCCATGTG	GCAACATTCT	9539
GTCAGCCTCT	TTCATAGTGT	GCAAACATTT	TATCATTTCTA	AATGGTGACT	CTCTGCCCTT	9599
GGACCCATTT	ATTATTCACA	GATGGGGAGA	ACCTATCTGC	ATGGACCCTC	ACCATCCTCT	9659
GTGCAGCACA	CACAGTGCAG	GGAGCCAGTG	GCGATGGCGA	TGACTTTCTT	CCCCTGGGAA	9719
TTCC						9723

146